

TITLE HIN-1, a putative cytokine highly expressed in normal but not
 JOURNAL Cancerous mammary epithelial cells
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9796-9801 (2001)
 PUBMED 21396515
 REFERENCE 2 (bases 1 to 461)
 AUTHORS Polyak, K., Krop, I. and Sgroi, D.
 JOURNAL Direct Submission
 TITLE Submitted (15-JUN-2001) Adult Oncology, Dana-Farber Cancer
 INSTITUTE, 44 Binney St. D740C, Boston, MA 02115, USA
 FEATURES Location/Qualifiers
 source 1..461
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /map="5q35-tel"
 CDS 22..336
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 /db_xref="GI:15079188"
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 Query Match 100.0%; Score 312; DB 9; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1.9e-39;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAGCTCGCGCCCTCTCGGGCTCTCGTGGCCCTCTCTCTGAGCTCCGCTCGTCT 60
 DB 22 ATGAAGCTCGCGCCCTCTCGGGCTCTCGTGGCCCTCTCTCTGAGCTCCGCTCGTCT 81
 QY 61 TTCTTAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCGTGGCTGGAGTCGGCGCG 120
 DB 82 TTCTTAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCGTGGCTGGAGTCGGCGCG 141
 QY 121 GAGGCGGGCGCGGACCTCGGCCAACCCCTCGGCACCCCTCAACCCGCTGAAGTCCTG 180
 DB 142 GAGGCGGGCGCGGACCTCGGCCAACCCCTCGGCACCCCTCAACCCGCTGAAGTCCTG 201
 QY 181 CTGACAGCTGGGCATCCCTGACACCTCATAGAGGCTCCAGAGTGTGGCT 240
 DB 202 CTGACAGCTGGGCATCCCTGACACCTCATAGAGGCTCCAGAGTGTGGCT 261
 QY 241 GAGCTGGGTCCCGAGCCGCTGGGGCCGCTGAAGCCCTGAAGCCCTGTGGGGCCCTG 300
 DB 262 GAGCTGGGTCCCGAGCCGCTGGGGCCGCTGAAGCCCTGTGGGGCCCTG 321
 QY 301 ACAGTGTGGC 312
 DB 322 ACAGTGTGGC 333
 RESULT 2
 AF436839
 LOCUS Homo sapiens pneumo secretory protein 2 mRNA, complete cds.
 DEFINITION
 ACCESSION AF436839
 VERSION AF436839.1 GI:33315289
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 461)
 AUTHORS Clippe, A., Laing, I.A., LeSueur, P.N., Bernard, A. and Knoop, B.
 TITLE Molecular cloning of PhSP-1, a protein of the respiratory tract
 with potential association to atopy
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 461)
 AUTHORS Clippe, A., Bernard, A. and Knoop, B.
 JOURNAL Direct Submission
 TITLE Submitted (22-OCT-2001) Unit of Toxicology, Catholic University of
 Louvain, Clos Chapelle-aux-Champs, 30.54, Brussels, B 1200, Belgium
 FEATURES Location/Qualifiers
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 Best Local Similarity 99.4%; Pred. No. 6e-39;
 Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAGCTCGCGCCCTCTCGGGCTCTCGTGGCCCTCTCTCTGAGCTCCGCTCGTCT 60
 DB 22 ATGAAGCTCGCGCCCTCTCGGGCTCTCGTGGCCCTCTCTCTGAGCTCCGCTCGTCT 81
 QY 61 TTCTTAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCGTGGCTGGAGTCGGCGCG 120
 DB 82 TTCTTAGTGGGCTCGGCCAAGCTGTGGCCAGCTGTGCGTGGCTGGAGTCGGCGCG 141
 QY 121 GAGGCGGGCGCGGACCTCGGCCAACCCCTCGGCACCCCTCAACCCGCTGAAGTCCTG 180
 DB 142 GAGGCGGGCGCGGACCTCGGCCAACCCCTCGGCACCCCTCAACCCGCTGAAGTCCTG 201
 QY 181 CTGACAGCTGGGCATCCCTGACACCTCATAGAGGCTCCAGAGTGTGGCT 240
 DB 202 CTGACAGCTGGGCATCCCTGACACCTCATAGAGGCTCCAGAGTGTGGCT 261
 QY 241 GAGCTGGGTCCCGAGCCGCTGGGGCCGCTGAAGCCCTGAAGCCCTGTGGGGCCCTG 300
 DB 262 GAGCTGGGTCCCGAGCCGCTGGGGCCGCTGAAGCCCTGTGGGGCCCTG 321
 QY 301 ACAGTGTGGC 312
 DB 322 ACAGTGTGGC 333
 RESULT 3
 HUMZB52D10
 LOCUS Homo sapiens full length insert cDNA clone ZB52D10.
 DEFINITION
 ACCESSION AF086152
 VERSION AF086152.1 GI:3483497
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 471)
 AUTHORS Woessner, J., Tan, F., Marra, M., Kucaba, T., Vandell, M., Martin, J.,
 Marth, G., Bowles, I., Wylie, T., Bowers, Y., Steptoe, M., Theising, B.,
 Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B.,
 Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R.,
 Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behymer, K., Hillier, L.,
 Wilson, R. and Waterston, R.
 TITLE Full Clone Sequencing of the Longest Available Member from Each
 Unigene Cluster
 JOURNAL Unpublished

/translation="MKLAALLGLCVLSCSAAFLVGSAPKPAOPVAALSAEAAAGA
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ORIGIN
Query Match 99.0%; Score 308.8; DB 9; Length 503;
Best Local Similarity 99.4%; Pred. No. 5.9e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGGCTCTCTGGGCTCTGCTGGCCCTGCTCTGAGCTCGCTGCTGCT 60
DB 16 ATGAAGCTCGCGGCTCTCTGGGCTCTGCTGGCCCTGCTCTGAGCTCGCTGCTGCT 75
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DB 76 TTCTTAGTGGCTCGGCAAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 135
QY 121 GAGCGCGGCGGACCTCTGGCCAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 180
DB 136 GAGCGCGGCGGACCTCTGGCCAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 195
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DB 196 CTGAGCAGCTCGGCAATCCCTGCTGAGCAACCTCTAGAGGCTTCAGAGTTCGGCT 255
QY 241 GAGCTGGTCCCGAGGCTCGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTG 300
DB 256 GAGCTGGTCCCGAGGCTCGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTG 315
QY 301 ACAGTGTGTTGGC 312
DB 316 ACAGTGTGTTGGC 327

RESULT 5
BD082142
LOCUS
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION BD082142
VERSION BD082142.1 GI:22627752
KEYWORDS JP 2001522225-A/6.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 519)
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE Reagents and methods useful for detecting diseases of the lung
JOURNAL ABBOTT LABORATORIES
COMMENT JP 2001522225-A 6 13-NOV-2001;
PD JP 2001522225-A/6
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA N FRIEDMAN,
PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI
PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
PI STROUPE
PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
CC Strandedness: Single;
Topology: Linear;
FH Key Location/Qualifiers
FT Location/Qualifiers
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ORIGIN
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Best Local Similarity 99.4%; Pred. No. 5.8e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGGCTCTCTGGGCTCTGCTGGCCCTGCTCTGAGCTCGCTGCTGCT 60
DB 79 ATGAAGCTCGCGGCTCTCTGGGCTCTGCTGGCCCTGCTCTGAGCTCGCTGCTGCT 138
QY 61 TTCTTAGTGGCTCGGCAAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 120
DB 139 TTCTTAGTGGCTCGGCAAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 198
QY 121 GAGCGCGGCGGACCTCTGGCCAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 180
DB 199 GAGCGCGGCGGACCTCTGGCCAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGGCG 258
QY 181 CTGAGCAGCTCGGCAATCCCTGCTGAGCAACCTCTAGAGGCTTCAGAGTTCGGCT 240
DB 259 CTGAGCAGCTCGGCAATCCCTGCTGAGCAACCTCTAGAGGCTTCAGAGTTCGGCT 318
QY 241 GAGCTGGTCCCGAGGCTCGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTG 300
DB 319 GAGCTGGTCCCGAGGCTCGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTG 378
QY 301 ACAGTGTGTTGGC 312
DB 379 ACAGTGTGTTGGC 390

RESULT 6
BD222719
LOCUS
DEFINITION Human signal peptide-containing protein.
ACCESSION BD222719
VERSION BD222719.1 GI:33032489
KEYWORDS JP 2002519030-A/65.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 543)
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Baughm,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C., Reddy,R., Hillman,J.L. and Bandman,O.
TITLE Human signal peptide-containing protein
JOURNAL Patent: JP 2002519030-A 65 02-JUL-2002;
COMMENT INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PD JP 2002519030-A/65
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/113129 PI PREETI
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,
PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
PC A61E25/00,
PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
C12N15/00,
PC A61K37/02,C12N5/00
CC Incyte Clone No: 3120415
FH Key Location/Qualifiers
FT source 1..543
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ORIGIN
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Best Local Similarity 99.4%; Pred. No. 5.7e-39;
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Db      122 ATGAAGCTCGCGCCCTCTCTGGGGCTCTGGGTGGCCCTGTCTGTGAGCTCCGCTGTGT 181
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QY      61 TTCTTAGTGGGCTCGGCCAGCCTGTGGGCCACGCTGTGCTGGCGTGGAGTCGGGGGG 120

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ORIGIN
Query Match          99.0%;   Score 108.8;   DB 6;   Length 543;
Best Local Similarity 99.4%;   Pred.No.5.8e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 1 ATGAAGTCGCCGCCCTCCTGGGGCTCTGGGTGGCCCTGCTCCTCAGCTCCGCTCGTCT 60
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Db 242 GAGCCGGGCGGGAGCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 301
Qy 181 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 302 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 361
Qy 241 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGCCCTCGTAAGGCCCTGCTGGGGCCCTG 300
Db 362 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGGCCCTGTAAGGCCCTGCTGGGGCCCTG 421
Qy 301 ACAGTGTGGC 312
Db 422 ACAGTGTGGC 433

RESULT 9
LOCUS AX201348 569 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 27 from Patent WO0153486.
ACCESSION AX201348
VERSION AX201348.1 GI:15391167
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hillan,K.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Stone,D.M., Watanabe,C.K., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Compositions and Methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 27 26-JUL-2001;
Genentech, Inc. (US)
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source 1..569
/mol_type="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 79 ATGAGCTCGCGCCCTCTGGGCTCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 138
Qy 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGGCTGCTGCTGCTGCT 120
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Qy 121 GAGCCGGGCGGGAGCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCCGGGCGGGAGCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 258
Qy 181 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 259 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
Qy 241 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGCCCTCGTAAGGCCCTGCTGGGGCCCTG 300
Db 319 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGCCCTCGTAAGGCCCTGCTGGGGCCCTG 378
Qy 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390

RESULT 11
LOCUS AX403520 570 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION AX403520
VERSION AX403520.1 GI:21437002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 407 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source 1..570
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ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
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Qy 1 ATGAGCTCGCGCCCTCTGGGCTCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 79 ATGAGCTCGCGCCCTCTGGGCTCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 138
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Qy 181 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 259 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
Qy 241 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGCCCTCGTAAGGCCCTGCTGGGGCCCTG 300
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Qy 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390
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RESULT 10
LOCUS AR252648 570 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 407 from patent US 6479825.
ACCESSION AR252648
VERSION AR252648.1 GI:27300556
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 570)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6479825-A 407 12-NOV-2002;
Genentech Inc. (US)
FEATURES
source 1..570
/mol_type="genomic DNA"
ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGGCTGCTGCTGCTGCT 120
Db 139 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGGCTGCTGCTGCTGCT 198
Qy 121 GAGCCGGGCGGGAGCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCCGGGCGGGAGCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 258
Qy 181 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 259 CTGAGCAGCTCGGCGATCCCGCTGAACACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
Qy 241 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGCCCTCGTAAGGCCCTGCTGGGGCCCTG 300
Db 319 GAGCTGGTCCCGAGGCGGTGGGGCCGCTGAAGCCCTCGTAAGGCCCTGCTGGGGCCCTG 378
Qy 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390

RESULT 11
LOCUS AX403520 570 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION AX403520
VERSION AX403520.1 GI:21437002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 407 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source 1..570
/mol_type="genomic DNA"
ORIGIN
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JOURNAL Submitted (16-OCT-2000) Laboratory of Metabolism, National Cancer
Institute, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES
source 1. .347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
11. .325
/codon_start=1
/product="UGRP2"
/protein_id="AAL26217.1"
/db_xref="GI:16565422"
/translaton="MKLAALGLCVALSAAFLVGSAPKVPVAPVALESABAGA
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VFG"
ORIGIN
Query Match 98.5%; Score 307.2; DB 9; Length 347;
Best Local Similarity 99.0%; Pred. No. 1.1e-38;
Matches 309; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAAGCTGGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60
Db 11 ATGAAGTGGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 70
QY 61 TTCTTAGTGGCTCGGCAAGCTCTGGCCAGCCTGTGGCTGGCTGGCTGGCTGGCTGG 120
Db 71 TTCTTAGTGGCTCGGCAAGCTCTGGCCAGCCTGTGGCTGGCTGGCTGGCTGGCTGG 130
QY 121 GAGCGCGGCGCGGACCTTGGCCAAACCCCTCGGCAACCTCAACCCCTGTAAGCTCTG 180
Db 131 GAGCGCGGCGCGGACCTTGGCCAAACCCCTCGGCAACCTCAACCCCTGTAAGCTCTG 190
QY 181 CTGAGCAGCTGGGCTATCCCTCGTGAACCACTCATAGAGGCTCCCAAGCTGTGGCT 240
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QY 241 GAGCTGGTCCCGAGGCGTGGGCGCGTGAAGCCCTGTAAGCCCTGCTGGGCGCCCTG 300
Db 251 GAGCTGGTCCCGAGGCGTGGGCGCGTGAAGCCCTGTAAGCCCTGCTGGGCGCCCTG 310
QY 301 ACAGTGTGTGGC 312
Db 311 ACAGTGTGTGGC 322
RESULT 14
AC108083 130129 bp DNA linear HTG 25-JAN-2002
LOCUS Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
DEFINITION SEQUENCE, 4 unordered pieces.
ACCESSION AC108083
VERSION AC108083.1 GI:18369929
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
DOE Joint Genome Institute.
Direct Submission
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
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Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 19292 bp in length
* 23713 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
FEATURES
source Location/Qualifiers
1. .130129
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2013L15"
/clone_lib="Caltech human BAC library D"
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Best Local Similarity 98.8%; Pred. No. 1.9e-28;
Matches 240; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 50 CCCTCGTCTTCTTTAGTGGCTCGGCCAAGCCTGTGGCCAGCCTGTGGCCAGCCTGTG 109
Db 49334 CAGCTGCTCTTCTTTAGTGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCGCTGG 49393
QY 110 AGTCGGCGGCGAGCGCGCGGACCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGC 169
Db 49394 AGTCGGCGGCGAGCGCGCGGACCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGC 49453
QY 170 TGAAGCTCTCTGTGAGCAGCCTGGGCATCCCGTGAACACCTCATAGAGGCTCCAGA 229
Db 49454 TGAAGCTCTCTGTGAGCAGCCTGGGCATCCCGTGAACACCTCATAGAGGCTCCAGA 49513
QY 230 AGTGTGTGGCTGAGCTGGGTCCCGAGCCCTGGGGCGCGTGAAGGCCCTCAAGGCCCTGC 289
Db 49514 AGTGTGTGGCTGAGCTGGGTCCCGAGCCCTGGGGCGCGTGAAGGCCCTCAAGGCCCTGC 49573
QY 290 TGG 292
Db 49574 TGG 49576
RESULT 15
AC106813 166777 bp DNA linear HTG 07-MAR-2002
LOCUS Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
DEFINITION 3 ordered pieces.
ACCESSION AC106813
VERSION AC106813.3 GI:19224876
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE

AUTHORS
TITLE
JOURNAL
REFERENCE

1 (bases 1 to 166777)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 166777)
DOE Joint Genome Institute.
Direct Submission
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 166777)
DOE Joint Genome Institute.
Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 7, 2002 this sequence version replaced gi:18369924.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1519801
Center clone name: RPCI-11_58619

Summary Statistics
Consensus quality: 163497 bases at least Q40
Consensus quality: 166071 bases at least Q30
Consensus quality: 166432 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 62237: contig of 62237 bp in length
* 62238 75837: gap of unknown length
* 62338 75837: contig of 13500 bp in length
* 75838 75937: gap of unknown length
* 75938 166777: contig of 90840 bp in length.

FEATURES

source

1..166777
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/mol_type="genomic DNA"
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/chromosome="5"
/clone="RP11-58619"
/clone_lib="RPCI human BAC library 11"

ORIGIN

Query Match 76.3%; Score 238.2; DB 2; Length 166777;
Best Local Similarity 98.8%; Pred No. 1.9e-28;
Matches 240; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 50 CGCTGCTGCTTTCTTAGTGGGCTCGGCAAGCCCTGTGGCCAGCCTGTGCTGGCTGG 109
DB 120260 CAGCTGCTGCTTTCTTAGTGGGCTCGGCAAGCCCTGTGGCCAGCCTGTGCTGGCTGG 120319
QY 110 AGTCGGCGCGAGGCGCGGCGCGGACCCCTGGCAACCCCTCGGACCCCTCAACCGC 169
DB 120320 AGTCGGCGCGAGGCGCGGCGCGGACCCCTGGCAACCCCTCGGACCCCTCAACCGC 120379
QY 170 TGAAGCTCTGCTGAGCAGCCTGGGCGATCCCGGTGAACCCACCTCATAGAGGCTCCCGAGA 229
DB 120380 TGAAGCTCTGCTGAGCAGCCTGGGCGATCCCGGTGAACCCACCTCATAGAGGCTCCCGAGA 120439
QY 230 AGTGTGTGGCTGAGCTGGGTCCCGAGGCGCGTGGGGCGGTGAAGGCCCTGAAGGCCCTGC 289

Db 120440 AGTGTGTGGCTGAGCTGGGTCCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGC 120499
QY 290 TGG 292
Db 120500 TGG 120502

Search completed: June 6, 2004, 14:59:41
Job time : 2270 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 09:57:16 ; Search time 340 seconds
(without alignments)
3898.346 Million cell updates/sec

Title: US-10-081-817A-3

Perfect score: 312

Sequence: 1 atgaagctgcgcgcctcct.....gggcccctgacagtgttggc 312

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1980s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.8	99.0	519	2	AAV54621 LU105 pol
2	308.8	99.0	543	3	Aaz29723 Human lun
3	308.8	99.0	543	3	Aaz298173 Human sig
4	308.8	99.0	561	9	Ade39936 Human lun
5	308.8	99.0	562	2	AAV54620
6	308.8	99.0	569	6	Abk40267 cDNA enco
7	308.8	99.0	570	3	Aaz65103 Membrane-
8	308.8	99.0	570	5	Aaf44249 Human PRO
9	308.8	99.0	570	7	Abx77974 Human PRO
10	308.8	99.0	570	7	Abx80386 Novel hum
11	308.8	99.0	570	7	Abx79570 Human sec
12	308.8	99.0	570	7	Abx90363 Human sec
13	308.8	99.0	570	7	Abx64209 cDNA enco
14	308.8	99.0	570	7	ACA64431 Novel hum
15	308.8	99.0	570	7	Abx80890 Human sec
16	308.8	99.0	570	7	ACD44399 cDNA enco
17	308.8	99.0	570	7	Abx79570 Human sec
18	308.8	99.0	570	7	ACA93591 Novel hum
19	308.8	99.0	570	7	Abx81273 Novel hum
20	308.8	99.0	570	7	ACA93089 Novel hum
21	308.8	99.0	570	7	Abx17173 Human PRO
22	308.8	99.0	570	8	ACA68028 Novel hum
23	308.8	99.0	570	8	ACA88477 Human sec

ALIGNMENTS

RESULT 1

AAV54621

ID AAV54621 standard; cDNA; 519 BP.

XX AC AAV54621;

XX 25-MAR-2003 (revised)

DT 30-OCT-1998 (first entry)

XX LU105 polypeptide encoding cDNA clone 1327836TH.

XX LU105; lung disease marker; immunoassay; lung disease; cancer; blood;

XX Plasma; serum; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 79..393

FT /**tag=a

FT /transl_except= (pos:136..138, aa:Val)

FT /product= "LU105 polypeptide"

XX WO9833926-A1.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US001766.

XX 31-JAN-1997; 97US-00791710.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

XX Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;

XX Russell JC, Stroupe SD;

XX WPI; 1998-437479/37.

XX P-PSDB; AAW75868.

XX New nucleic acid for the lung disease marker LU105 - polypeptides,

XX antibodies and genes, used for diagnosis, prevention, treatment of lung

XX disease, specifically cancer.

XX Claim 11; Fig 1; 123pp; English.

XX Sequences shown in AAV54616 to AAV54621 represent LU105 specific

Acdb1984 cDNA enco
Ada37918 Human cDN
Ada21604 Human cDN
Ada10391 Human cDN
Ada17935 cDNA enco
Ada28043 Human cDN
Ada94623 Human cDN
Ada38848 Human cDN
Ada92969 Human cDN
Ach65545 Human cDN
Ada2530 Human cDN
Acdb39535 Human cDN
Ada06696 Human sec
Ada39389 Human cDN
Adb96415 Human PRO
Adc57887 Human PRO
Adc55251 Human PRO
Adc12118 Human cDN
Adc56540 Human PRO
Adc07595 Human cDN
Adc11585 Human cDN
Adc14707 Novel hum

CC polynucleotide sequences. These are used in the method of the invention
CC for detecting target LUI05 nucleic acid. The method comprises treating a
CC sample with at least one LUI05 specific nucleic acid, or its complement
CC which is at least 50 percent identical with the LUI05 specific nucleic
CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.
CC Cells transformed with a recombinant expression system that contains
CC LUI05 specific nucleic acid fragments, are used to express recombinant
CC LUI05 polypeptides which are used to raise antibodies. The antibodies are
CC used to detect the LUI05 antigen, and correspondingly this antigen is
CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
CC monitoring, prognosis, prevention, treatment and determination of
CC susceptibility to, lung disease, specifically cancer. The LUI05
CC polypeptides are also used to screen for specific binding agents, useful
CC therapeutically. LUI05 is a marker for lung disease (present at high
CC concentration, in altered form or in an unusual body compartment) LUI05
CC can be detected in blood, plasma or serum in an inexpensive, non-invasive
CC test. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 2; Length 519;
Best Local Similarity 99.4%; Pred. No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60
Db 79 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 138
Qy 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 139 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 198
Qy 121 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 180
Db 199 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 258
Qy 181 CTGAGAGCTGGGCATCCCTGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 259 CTGAGAGCTGGGCATCCCTGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
Qy 241 GAGCTGGTCCCGAGGCGTGGGGCGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 300
Db 319 GAGCTGGTCCCGAGGCGTGGGGCGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 378
Qy 301 ACAGTGTGTGGC 312
Db 379 ACAGTGTGTGGC 390

RESULT 2
AAZ29723
ID AAZ29723 standard; DNA; 543 BP.

AC AAZ29723;

DT 27-MAR-2000 (first entry)

XX Human lung specific gene Lngl07.

XX Lung Specific Gene; LSG; Lngl07; human; diagnostic marker; prognosticate;
XX lung cancer; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 93..407
XX FT /*tag= a
XX FT /product= "LSG Lngl07 protein"

XX W09960160-A1.

XX 25-NOV-1999.

XX 12-MAY-1999; 99WO-US010344.
XX 21-MAY-1998; 98US-0086212P.
XX (DIAD-) DIADEXUS LLC.
XX Yang F, Macina RA, Sun Y;
XX WPI; 2000-116320/10.
XX P-PSDB; AAY4458.
XX A new method for diagnosing, monitoring and staging lung cancer.
XX Claim 6; Page 36; 40pp; English.
XX The present sequence is a lung specific gene (LSG) Lngl07 from human
XX clone ID 586271. The LSG has high level of tissue specificity for lungs
XX and is overexpressed in cancerous tissues. The sequence serves as a
XX diagnostic marker for detecting, monitoring, staging and prognosticating
XX lung cancer. The diagnosis involves comparing levels of LSG in samples
XX obtained from patient and normal control.

XX Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 3; Length 543;
Best Local Similarity 99.4%; Pred. No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60
Db 93 ATGAAGCTCGCGCCCTCTCTGGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 152
Qy 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 153 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 212
Qy 121 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 180
Db 213 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 272
Qy 181 CTGAGAGCTGGGCATCCCTGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 273 CTGAGAGCTGGGCATCCCTGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 332
Qy 241 GAGCTGGTCCCGAGGCGTGGGGCGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 300
Db 333 GAGCTGGTCCCGAGGCGTGGGGCGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 392
Qy 301 ACAGTGTGTGGC 312
Db 393 ACAGTGTGTGGC 404

RESULT 3

AAZ98173
ID AAZ98173 standard; cDNA; 543 BP.

XX AAZ98173;

XX 11-MAY-2000 (first entry)

XX Human signal peptide containing protein HSP65-65 cDNA SEQ ID NO:199.

XX Human; signal peptide-containing protein; HSP65; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's disease; ovulatory defect;
XX muscular dystrophy; ss.

XX Homo sapiens.
OS WO20000610-A2.
PN XX
XX 06-JAN-2000.
XX 25-JUN-1999; 99WO-US014484.
XX 26-JUN-1998; 98US-0090762P.
PR 31-JUL-1998; 98US-0094983P.
PR 01-OCT-1998; 98US-0102686P.
PR 11-DEC-1998; 98US-0112129P.
XX (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX WPI; 2000-160673/14.
DR P-PSDB; AAY87288.
XX
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.
XX
XX Claim 9; Page 289; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
CC used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPP. Antagonists of
CC HSPP are used to treat or prevent disorders associated with increased
CC activity or function of HSPP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC nucleic acids can be used for the recombinant production of HSPP, for
CC detecting HSPP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSPP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSPP from natural
XX sources
XX
XX Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;
SQ
Query Match 99.0%; Score 308.8; DB 3; Length 543;
Best Local Similarity 99.4%; Pred. No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCCCGCCCTCTCTGGGGCTCTGGTGGCCCTGTCTGACAGCTCCGCTCGTGTCT 60
DB 93 ATGAAGCTCCCGCCCTCTCTGGGGCTCTGGTGGCCCTGTCTGACAGCTCCGCTCGTGTCT 152
QY 61 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCTGTGCTGCTGTGGAGTGGGGGG 120
DB 153 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCTGTGCTGCTGTGGAGTGGGGGG 212
QY 121 GAGCCGGGGCGGGACCTGGCCACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 180
DB 213 GAGCCGGGGCGGGACCTGGCCACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 272
QY 181 CTGAGCAGCTGGGATCCCGTGAACCACTCATAGAGGGCTCCCAAGAGTGTGTGGCT 240

DB 273 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGGCTCCCAAGTGTGTGGCT 332
QY 241 GAGCTGGTCCCGAGCCCTGGGGCCCTGAGAGCCCTGAAGCCCTGCTGGGGGGCCCTG 300
DB 333 GAGCTGGTCCCGAGCCCTGGGGCCCTGAGAGCCCTGAAGCCCTGCTGGGGGGCCCTG 392
QY 301 ACAGTGTGGG 312
DB 393 ACAGTGTGGG 404
RESULT 4
ID ADE39936
ID ADE39936 standard; cDNA; 561 BP.
XX
AC ADE39936;
XX
DT 29-JAN-2004 (first entry)
XX
XX Human lung disorder-related cDNA - SEQ ID 6.
DE
XX pepsin C; lung disorder; human; ss.
XX
XX Homo sapiens.
XX
XX US2003124580-A1.
XX
XX 03-JUL-2003.
XX
XX 06-SEP-2002; 2002US-00237435.
XX
XX 07-SEP-2001; 2001US-0317822P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Walker MG, Spiro PA, Murry LE;
PI WPI; 2003-810982/76.
XX
XX New cDNAs co-expressed with lung surfactant and surfactant synthesis
PT genes, useful as diagnostics in assessing the prognosis and treatment of
PT a lung disorder, or as potential targets for identifying therapeutics for
PT lung disorders.
XX
XX Claim 2; SEQ ID NO 6; 29pp; English.
XX
XX The invention relates to a novel isolated cDNA and a cDNA encoding pepsin
CC C. The polynucleotide of the invention may be useful as a probe or a
CC component within an expression vector, as a diagnostic in assessing the
CC prognosis and treatment of a lung disorder and as a potential therapeutic
CC or target for the identification of therapeutics for lung disorders.
CC Furthermore, the polynucleotide may be used to produce purified proteins
CC or peptides which can subsequently be used to produce antibodies. The
CC current sequence is that of the human lung disorder-related cDNA (SEQ ID
CC 6) of the invention.
XX
XX Sequence 561 BP; 86 A; 200 C; 189 G; 86 T; 0 U; 0 Other;
SQ
Query Match 99.0%; Score 308.8; DB 9; Length 561;
Best Local Similarity 99.4%; Pred. No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCCCGCCCTCTCTGGGGCTCTGGTGGCCCTGTCTGACAGCTCCGCTCGTGTCT 60
DB 117 ATGAAGCTCCCGCCCTCTCTGGGGCTCTGGTGGCCCTGTCTGACAGCTCCGCTCGTGTCT 176
QY 61 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCTGTGCTGCTGGAGTGGGGGG 120
DB 177 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCTGTGCTGCTGGAGTGGGGGG 236
QY 121 GAGCCGGGGCGGGACCTGGCCACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 180

Db 237 GAGGCGGGCGGGACCCCTGCGCCACCCCTCGCACCCCTCAACCCGCTGAAGCTCTG 296
 QY 181 CTCAGCAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCAGAGGTGTGGCT 240
 Db 297 CTGAGCAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCAGAGGTGTGGCT 356
 QY 241 GAGCTGGGTCCCGCAGCCCTGCGGGCGGTGAAGGCCCTGAAGGCCCTGCTGGGGCCCTG 300
 Db 357 GAGCTGGGTCCCGCAGCCCTGCGGGCGGTGAAGGCCCTGAAGGCCCTGCTGGGGCCCTG 416
 QY 301 ACAGTGTGTGGC 312
 Db 417 ACAGTGTGTGGC 428
 RESULT 5
 AAV54620
 ID AAV54620 standard; cDNA; 562 BP.
 AC AAV54620;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-OCT-1998 (first entry)
 XX
 DE LU105 specific consensus polynucleotide sequence.
 XX
 KW LU105; lung disease marker; immunoassay; lung disease; cancer; blood;
 KW plasma; serum; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 122..436
 FT CDS /*tag= a
 FT /transl_except= (pos:176..178, aa:Val)
 FT /product= "LU105 polypeptide"
 XX
 PN WO9833926-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US001766.
 XX
 PR 31-JAN-1997; 97US-00791710.
 XX
 PA (ABEO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PM, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;
 PI Russell JC, Stroupe SD;
 XX
 DR WPI; 1998-437479/37.
 DR P-PSDB; AAW75868.
 XX
 PT New nucleic acid for the lung disease marker LU105 - polypeptides,
 PT antibodies and genes, used for diagnosis, prevention, treatment of lung
 PT disease, specifically cancer.
 XX
 PS Claim 11; Fig 1; 123pp; English.
 XX
 CC Sequences shown in AAV54616 to AAV54621 represent LU105 specific
 CC polynucleotide sequences. These are used in the method of the invention
 CC for detecting target LU105 nucleic acid. The method comprises treating a
 CC sample with at least one LU105 specific nucleic acid, or its complement
 CC which is at least 50 percent identical with the LU105 specific nucleic
 CC acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker.
 CC Cells transformed with a recombinant expression system that contains
 CC LU105 specific nucleic acid fragments, are used to express recombinant
 CC LU105 polypeptides which are used to raise antibodies. The antibodies are
 CC used to detect the LU105 antigen, and correspondingly this antigen is
 CC used to detect specific antibodies, in usual immunoassays. The LU105
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
 CC monitoring, prognosis, prevention, treatment and determination of

CC susceptibility to, lung disease, specifically cancer. The LU105
 CC polypeptides are also used to screen for specific binding agents, useful
 CC therapeutically. LU105 is a marker for lung disease (present at high
 CC concentration, in altered form or in an unusual body compartment). LU105
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive
 CC test. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 0 U; 2 Other;
 Query Match 99.0%; Score 308.8; DB 2; Length 562;
 Best Local Similarity 99.4%; Pred. No. 4.3e-53;
 Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAGCTCGCGCCCTCCTCGGGCTCTGCGTGGCCCTGCTGCTGAGCTCGCTGCT 60
 Db 122 ATGAAGCTCGCGCCCTCCTCGGGCTCTGCGTGGCCCTGCTGCTGAGCTCGCTGCT 181
 QY 61 TTCTTAGTGGCTCGGCCAAGCCTGTGCGCCAGCCTGTGCGTGGCTGGAGTCGCGCGCG 120
 Db 182 TTCTTAGTGGCTCGGCCAAGCCTGTGCGCCAGCCTGTGCGTGGCTGGAGTCGCGCGCG 241
 QY 121 GAGCGCGGGCGGAGCCCTGCGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCTG 180
 Db 242 GAGCGCGGGCGGAGCCCTGCGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCTG 301
 QY 181 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGGTGTGGCT 240
 Db 302 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGGTGTGGCT 361
 QY 241 GAGCTGGGTCCCCAGGCGCTGGGGCGCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300
 Db 362 GAGCTGGGTCCCCAGGCGCTGGGGCGCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 421
 QY 301 ACAGTGTGTGGC 312
 Db 422 ACAGTGTGTGGC 433
 RESULT 6
 ABK40267
 ID ABK40267 standard; cDNA; 569 BP.
 XX
 AC ABK40267;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE cDNA encoding human PRO1245 polypeptide.
 XX
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cytostatic; neuroprotective; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153486-A1.
 XX
 PD 26-JUL-2001.
 XX
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XX		(GETH) GENENTECH INC.	
XX	PA	Baker K, Chen J, Goddard A., Gurney AL, Smith V, Watanabe CK;	
XX	PI	Wood WI, Yuan J;	
XX	PI	WPI; 2000-072883/06.	
XX	DR	P-PSDB; AAY66757.	
XX	PT	Membrane-bound proteins and related nucleotide sequences.	
XX	PT	Claim 2; Fig 289; 822pp; English.	
XX	PS	The invention provides membrane-bound PRO polypeptides and	
XX	PS	polynucleotides encoding them. The PRO sequences of the invention were	
CC	CC	identified based on extracellular domain homology screening. The PRO	
CC	CC	sequences have homology with proteins including LDL receptors, TIE	
CC	CC	ligands and various enzymes. The membrane-bound proteins and receptor	
CC	CC	molecules are useful as pharmaceutical and diagnostic agents. Receptor	
CC	CC	immunoadhesins, for instance, can be used as therapeutic agents to block	
CC	CC	receptor-ligand interactions. The membrane-bound proteins can also be	
CC	CC	employed for screening of potential peptide or small molecule inhibitors	
CC	CC	of the relevant receptor/ligand interaction. The PRO encoding sequences	
CC	CC	are useful as hybridization probes, in chromosome and gene mapping and in	
CC	CC	the generation of antisense RNA and DNA. PRO nucleic acid sequences will	
CC	CC	also be useful for the preparation of PRO polypeptides, especially by	
CC	CC	recombinant techniques	
XX	SQ	Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;	
		Query Match 99.0%; Score 308.8; DB 3; Length 570;	
		Best Local Similarity 99.4%; Pred. No. 4.3e-53;	
		Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1	ATGAGCTCGCGGCCTCCTGGGCTCTGGTGGGCCCTGTCTGCAGCTCGGTCGTGCT 60	
Db	79	ATGAAGCTCGCGGCCTCCTGGGCTCTGGTGGGCCCTGTCTGCAGCTCGGTCGTGCT 138	
QY	61	TTCCTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCTGGAGTCGGCGGCG 120	
Db	139	TTCCTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGTGGAATCGCGGCG 198	
QY	121	GAGGCGGGGCGGACCTCGGCCAAACCCCTCGGACCCTCAACCCGCTGAAGCTCCTG 180	
Db	199	GAGGCGGGGCGGACCTCGGCCAAACCCCTCGGACCCTCAACCCGCTGAAGCTCCTG 258	
QY	181	CTGAGCAGCTCGGCATCCCCGTGAACCACTCATAGAGGSGTCCCAGAAGTGTGTGGCT 240	
Db	259	CTGAGCAGCTCGGCATCCCCGTGAACCACTCATAGAGGCTCCCAAGAATGTGTGGCT 318	
QY	241	GAGCTGGGTCCCAGCGCGTGGGGCCGTGAAGGCCCTGTGCTGGGGGCGGCTG 300	
Db	319	GAGCTGGGTCCCAGCGCGTGGGGCCGTGAAGGCCCTGTGCTGGGGGCGGCTG 378	
QY	301	ACAGTGTTTGGC 312	
Db	379	ACAGTGTTTGGC 390	
RESULT 8			
AAF44249			
ID	AAF44249	standard; cDNA; 570 BP.	
XC	AAF44249;		
AC			
XX			
DT	02-APR-2001	(first entry)	
XX			
DE	Human PRO1245	nucleotide sequence SEQ ID NO:407.	
XX			
KW	Human; secreted and transmembrane protein; PRO; cytotstatic; cell death;		
KW	cancer; chromosomal mapping; gene mapping; tissue typing;		
KW	diagnostic assay; ss.		
XX			

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OS Homo sapiens.
XX WO200073454-A1.
XX PD 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US008439.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
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XX 28-JUL-1999; 99US-0146222P.
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XX 06-JAN-2000; 2000WO-US000376.
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XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
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XX 15-MAR-2000; 2000WO-US006884.
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XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX WPI; 2001-032160/04.
XX PD P-PSDB; AAB65280.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 2; Fig 289; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX AAB65300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention
XX
XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
XX
XX Query Match 99.0%; Score 308.8; DB 5; Length 570;
XX Best Local Similarity 99.4%; Pred. No. 4.3e-53;
XX Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ATGAAGCTCGCCCTCTCGTGGGCTCTCGTGGCCCTGCTCGAGCTCCGCTCGTCTGCT 60
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db 199 GAGGCCGGGGCGGGGACCCCTGCGCCAAACCCCTCGGCACACCCCTCAACCCGCTGAAGCTCCCTG 258
QY 181 CTGAGCAGCCTGGGCATCCCCGTGAACCACTCAATAGAGGGCTCCAGAGTGTGTGGCT 240
Db 259 CTGAGCAGCCTGGGCATCCCCGTGAACCACTCAATAGAGGGCTCCAGAGTGTGTGGCT 318
QY 241 GAGCTGGGTCCCCAGGCGCGTGGGGCGCGTGAAGGCCCTGTAAGGCCCTGCTGGGGGCCCTG 300
Db 319 GAGCTGGGTCCCCAGGCGCGTGGGGCGCGTGAAGGCCCTGTAAGGCCCTGCTGGGGGCCCTG 378
QY 301 ACAGTGTGTGGC 312
Db 379 ACAGTGTGTGGC 390
XX
XX RESULT 9
XX ABX77974
XX ID ABX77974 standard; cDNA; 570 BP.
XX AC ABX77974;
XX XX
XX DT 14-APR-2003 (first entry)
XX DE Human PRO polynucleotide #127.
XX KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
XX KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XX KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX XX
XX PN US2003027163-A1.
XX XX
XX PD 06-FEB-2003.
XX XX
XX PF 15-NOV-2001; 2001US-00997666.
XX XX
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XX PR 04-JUN-1998; 98US-0088033P.
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XX PR 05-JUN-1998; 98US-0088217P.
XX PR 09-JUN-1998; 98US-0088655P.

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 XX (GETH) GENENTECH INC.

XX PA
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan U, Paoni NP;
 PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams EW, Wood WI;
 PI Zhang Z;
 XX

DR WPI; 2003-247083/24.
 DR P-PSDB; ABU59174.
 DR

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 XX are therapeutically useful for enhancing immune response and in cancer
 XX treatments.
 XX

XX Claim 2; Fig 291; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
 XX polypeptides are useful in detecting PRO polypeptides in a sample, in
 XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 XX in modulating at least one biological activity of a cell expressing a PRO
 XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 XX useful for treating cardiac insufficiency disorders. PRO154 and PRO186
 XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
 XX PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 XX useful for treating conditions or disorders where angiogenesis would be
 XX beneficial, e.g. wound healing and antagonist of this polypeptide are
 XX useful for treating cancerous tumours. PRO812 inhibits vascular
 XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
 XX cells and is thus useful for inhibiting endothelial cell growth in
 XX mammals which would be beneficial in inhibiting tumour growth. PRO826,
 XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 XX stimulated T-lymphocytes and are therapeutically useful for enhancing
 XX immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 XX rod photoreceptor cells) and therefore are useful for treating retinal
 XX disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
 XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 XX and therefore are useful for treating kidney disorders associated with
 XX decreased mesangial cell function such as Berger disease or other
 XX nephropathies associated with dermatitis, herpeticiformis or Crohn's
 XX disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 XX proliferation and/or redifferentiation of chondrocytes in culture and are
 XX thus useful for treating sports injuries, and arthritis. This sequence
 XX represents a novel human PRO protein polynucleotide

XX SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.6; DB 7; Length 570;
 Best Local Similarity 99.4%; Pred. No. 4.3e-53;
 Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTCTCTCAGCTCGCTCGTCTGCT 60
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Db 139 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGCTGGCTGGAGTGGGGGCG 198
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 Db 199 GAGCGCGGGCCCGGAGCCCTGTGGCCAAACCCCTCGGCACCCCTCAACCGCTGAAGCTCTCTG 258
 QY 181 CTGAGCAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
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 Db 259 CTGAGCAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
 QY 241 GAGCTGGTCCCGCAGGCGCTGGGGGCGCTGAAGGCGCTGAAGGCGCTGTGGGGGCGCTG 300
 |||||
 Db 319 GAGCTGGTCCCGCAGGCGCTGGGGGCGCTGAAGGCGCTGTGGGGGCGCTG 378
 QY 301 ACAAGTGTGGC 312
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 Db 379 ACAAGTGTGGC 390
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 ID ACA69292
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 AC ACA69292;
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 DT 26-JUN-2003 (first entry)
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 KW cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosum; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.
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 OS Homo sapiens.
 XX
 FN US2003032023-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 14-NOV-2001; 2001US-00990711.
 XX
 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 25-NOV-1997; 97US-0066770P.
 PR 24-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
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 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.


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PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089972P.
PR 16-SEP-1998; 98WO-US019330.
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PR 01-DEC-1998; 98WO-US025108.
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PR 08-JAN-1999; 98WO-US028634.
PR 08-MAR-1999; 98WO-US005028.
PR 02-JUN-1999; 98WO-US012252.
PR 15-SEP-1999; 98WO-US021090.
PR 13-SEP-1999; 98WO-US021547.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
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PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
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PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2000WO-US006520.
PR 01-JUN-2001; 2001WO-US0017800.

20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.
(GETH ) GENENTECH INC.
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski RJ;
Grimaldi JC, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;
WPI; 2003-352829/33.
P-PSDB; ABU72571.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
disease.
XX
PS Claim 1; Fig 289; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
209439, 203135, etc); or a sequence with at least 80% identity to a DNA
encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
are particularly useful for detecting or treating e.g. malignancies or
cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
disease in mammals. The PRO polypeptides are useful in drug screening,
particularly as targets for therapeutic intervention in these diseases,
and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
chromosome identification. The PRO genes are useful as hybridisation
probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
replacing a defective gene. This sequence encodes a novel human secreted
and transmembrane PRO polypeptide
XX
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 7; Length 570;
Best Local Similarity 99.4%; Pred.No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCCGCCCTCCTCGGGGCTCTGGTGGCCCTCTCTGCGAGCTCGCTCGTGTGCT 60
Db 79 ATGAAGCTCGCCGCCCTCCTCGGGGCTCTGGTGGCCCTCTCTGCGAGCTCGCTCGTGTGCT 138
QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCACGCTGTGCGCTGAGTGGGGCG 120
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QY 181 CTGAGCAGCTGGGGCATCCCGTGAAACCCACCTCATAGAGGGCTCCCAAGTGTGTGGCT 240
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DT	22-APR-2003 (first entry)
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KW	Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW	diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;
KW	tumour-associated antigenic target; TAR; ADERT;
KW	antibody-dependent enzyme mediated prodrug therapy; cytostatic.
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OS	Homo sapiens.
XX	
US	US2003027162-A1.
XX	
PD	06-FEB-2003.
XX	
PF	15-NOV-2001; 2001US-00997428.
XX	
PR	16-JUN-1997; 97US-0049787P.
PR	17-OCT-1997; 97US-0062250P.
PR	05-NOV-1997; 97WO-US020069.
PR	12-NOV-1997; 97US-0065186P.
PR	13-NOV-1997; 97US-0065311P.
PR	24-NOV-1997; 97US-0066770P.
PR	25-FEB-1998; 98US-0075945P.
PR	20-MAR-1998; 98US-0078910P.
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PR 28-JUL-1999; 98US-0146222P.
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PR 15-SEP-1999; 98WO-US021090.
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PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
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Best Local Similarity 99.4%; Pred. No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTGCGCCCTCTCGGGGCTCTGGGGCTGTGGGCTGTCTGTGAGCTCCGCTCGTCTGCT 60
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Db 139 TTCTTAGTGGCTCGGCCAGCCTGTGGCCAGCCTGTGCTGCTGAGTCCGCGGGG 198

QY 121 GAGCGCGGGCGGGGACCCCTGGGCAACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 180
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Search completed: June 6, 2004, 14:21:42
Job time : 344 secs

FEATURES

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ORIGIN

Query Match 99.0%; Score 308.8; DB 12; Length 473;
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 473)
 NIH-MGC <http://mgi.nhl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES

source Location/Qualifiers
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 /lab_host="DH10B"
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 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 99.0%; Score 308.8; DB 12; Length 473;
 Best Local Similarity 99.4%; Pred. No. 2.4e-42;
 Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAGCTCGCGCCCTCTGGGCTCTGCTGGCCCTGCTGCAGCTCGCTCGTCT 60
 Db 7 ATGAAGCTCGCGCCCTCTGGGCTCTGCTGGCCCTGCTGCAGCTCGCTCGTCT 66

Qy 61 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCTGTGGCTGGCTGGAGTCGGCGG 120
 Db 67 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCTGTGGCTGGCTGGAGTCGGCGG 126

Qy 121 GAGCGCGGGCGGACCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTCAAGCTCCTG 180
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Qy 181 CTGAGCAGCTCGGGCATCCCGTGAACACCACTCATAGAGGCTCCAGAGTGTGGCT 240
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Qy 241 GAGCTGGTCCCGAGGCGTGGGGCCGTGAAGCCCTGAAGGCGCTGCTGGGGCCCTG 300
 Db 247 GAGCTGGTCCCGAGGCGTGGGGCCGTGAAGCCCTGAAGGCGCTGCTGGGGCCCTG 306

Qy 301 ACAGTGTGGC 312
 Db 307 ACAGTGTGGC 318

RESULT 3

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ACCESSION BM977626
 VERSION BM977626.1 GI:19596235
 KEYWORDS EST.
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 1 (bases 1 to 490)
 Bonaudo, M.F.; Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL 97044477
 MEDLINE 889548
 PUBMED
 COMMENT Contact: McCray, PB
 McCray Lab

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 459-484, >GC rich#low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .490
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-CF-EN1-aef-o-13-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN
Query Match 99.0%; Score 308.8; DB 12; Length 490;
Best Local Similarity 99.4%; Pred. No. 2.5e-42;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGGTGCCCTGTCTCGAGCTCGCTCGTGTCT 60
458 ATGAAGCTCGCGCCCTCTGGGGCTCTGGTGCCCTGTCTCGAGCTCGCTCGTGTCT 399
QY 61 TTCTTAGTGGGCTCGGCAAGCTGTGGCCAGCCTGTGCTGCTGGTGGAGTCGGCGGCG 120
398 TTCTTAGTGGGCTCGGCAAGCTGTGGCCAGCCTGTGCTGCTGGTGGAGTCGGCGGCG 339
QY 121 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180
338 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 279
QY 181 CTGAGCAGCTCGGCAATCCCGTGAACACCATCTATAGAGGCTCCCGAGAGTGTGTGGCT 240
278 CTGAGCAGCTCGGCAATCCCGTGAACACCATCTATAGAGGCTCCCGAGAGTGTGTGGCT 219
QY 241 GAGCTGGTCCCGAGGCGTGGGGCCGTGAAGCCCTGAAGGCCCTGTGCGGGGCCCTG 300
218 GAGCTGGTCCCGAGGCGTGGGGCCGTGAAGGCCCTGTGCGGGGCCCTG 159
QY 301 ACAGTGTGGC 312
|||||

Db 158 ACAGTGTGGC 147

RESULT 4
BI818715
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI818715 496 bp mRNA linear EST 04-OCT-2001
60307535F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178608 5',
mRNA sequence.
BI818715
BI818715.1 GI:15930265
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11445 row: e column: 09
High quality sequence stop: 471.
Location/Qualifiers
1. .496
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:5178608"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN
Query Match 99.0%; Score 308.8; DB 12; Length 496;
Best Local Similarity 99.4%; Pred. No. 2.5e-42;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGGTGCCCTGTCTCGAGCTCGCTCGTGTCT 60
24 ATGAAGCTCGCGCCCTCTGGGGCTCTGGTGCCCTGTCTCGAGCTCGCTCGTGTCT 83
QY 61 TTCTTAGTGGGCTCGGCAAGCTGTGGCCAGCCTGTGCTGCTGGTGGAGTCGGCGGCG 120
84 TTCTTAGTGGGCTCGGCAAGCTGTGGCCAGCCTGTGCTGCTGGTGGAGTCGGCGGCG 143
QY 121 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180
144 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 203
QY 181 CTGAGCAGCTCGGCAATCCCGTGAACACCATCTATAGAGGCTCCCGAGAGTGTGTGGCT 240
204 CTGAGCAGCTCGGCAATCCCGTGAACACCATCTATAGAGGCTCCCGAGAGTGTGTGGCT 263
QY 241 GAGCTGGTCCCGAGGCGTGGGGCCGTGAAGCCCTGAAGGCCCTGTGCGGGGCCCTG 300
264 GAGCTGGTCCCGAGGCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGTGCGGGGCCCTG 323
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QY 301 ACAGTGTGGC 312
Db 324 ACAGTGTGGC 335

RESULT 5
BI769722 1004 bp mRNA linear EST 25-SEP-2001
LOCUS 60305021F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204452 5',
DEFINITION mRNA sequence.
ACCESSION BI769722
VERSION BI769722.1 GI:15761287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1512 row: j column: 05
High quality sequence start: 3
High quality sequence stop: 416
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Location/Qualifiers
1..1004
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5204452"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 99.0%; Score 308.8; DB 12; Length 1004;
Best Local Similarity 99.4%; Pred. No. 3e-42;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTCGTGGGCTCTCGTGGCCAGCTGTGCGTGGAGTCGCGCGG 60
Db 23 ATGAAGCTCGCGCCCTCTCGTGGGCTCTCGTGGCCAGCTGTGCGTGGAGTCGCTGCT 82
QY 61 TTCTTAGTGGCTCGGCCAAGCTGTGCGCCAGCTGTGCGTGGAGTCGCGCGG 120
Db 83 TTCTTAGTGGCTCGGCCAAGCTGTGCGCCAGCTGTGCGTGGAGTCGCGCGG 142
QY 121 GAGGCGGGGCGGACCCCTGCGCAACCCCTCGGCAACCCCTCAACCGCTGAAGTCCTG 180
Db 143 GAGGCGGGGCGGACCCCTGCGCAACCCCTCGGCAACCCCTCAACCGCTGAAGTCCTG 202
QY 181 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGGCTCCACAGAGTGTGCTG 240
Db 203 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGGCTCCACAGAGTGTGCTG 262

us-10-081-817a-3.rst

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QY 181 CTGAGCAGCTGGGATCCCCCGTGAACACCTCATAGAGGGCTCCAGAAAGTGTGTGGCT 240
Db 203 CTGAGCAGCTGGGATCCCCCGTGAACACCTCATAGAGGGCTCCAGAAAGTGTGTGGCT 262
QY 241 GAGCTGGTCCCCAGGCTGGGGCCGTGAGGCCCTGAAGCCCTGTGGGGGCCCTG 300
Db 263 GAGCTGGTCCCCAGGCTGGGGCCGTGAGGCCCTGAAGGCCCTGTGGGGGCCCTG 322
QY 301 ACAGTGTTTGGC 312
Db 323 ACAGTGTTTGGC 334

RESULT 7
LOCUS BM921624 1083 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6707854 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753142
5', mRNA sequence.
ACCESSION BM921624
VERSION BM921624.1 GI:19372003
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1083)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bglb-nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12788 row: h column: 07
High quality sequence stop: 486.
FEATURES
source
1..1083
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5753142"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 99.0%; Score 308.8; DB 12; Length 1083;
Best Local Similarity 99.4%; Pred. No. 3e-42;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGCTCGCGCCCTCCCTGGGCTGTGGCTGGCCCTGTCTGCTGACCTCGGCTCGTGT 60
Db 41 ATGAGCTCGCGCCCTCCCTGGGCTGTGGCTGGCCCTGTCTGCTGACCTCGGCTCGTGT 100
QY 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCCTGTGCTGCTGCTGAGTGTGGCGG 120
Db 101 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCCTGTGCTGCTGAGTGTGGCGG 160
QY 121 GAGGCCGGGCGCGGACCTGTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180

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Db 161 GAGGCCGGGCGCGGACCTGTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 220
QY 181 CTGAGCAGCTGGGATCCCCCGTGAACACCTCATAGAGGGCTCCAGAAAGTGTGTGGCT 240
Db 221 CTGAGCAGCTGGGATCCCCCGTGAACACCTCATAGAGGGCTCCAGAAAGTGTGTGGCT 280
QY 241 GAGCTGGTCCCCAGGCTGGGGCCGTGAGGCCCTGAAGGCCCTGTGGGGGCCCTG 300
Db 281 GAGCTGGTCCCCAGGCTGGGGCCGTGAGGCCCTGAAGGCCCTGTGGGGGCCCTG 340
QY 301 ACAGTGTTTGGC 312
Db 341 ACAGTGTTTGGC 352

RESULT 8
LOCUS AW974727 550 bp mRNA linear EST 02-JUN-2000
DEFINITION EST386817 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
ACCESSION AW974727
VERSION AW974727.1 GI:8165915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, J. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 338
Seq primer: Reverse.
Location/Qualifiers
1..550
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pBluescriptSKm"

ORIGIN
Query Match 98.5%; Score 307.2; DB 10; Length 550;
Best Local Similarity 99.0%; Pred. No. 4.7e-42;
Matches 309; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGCTCGCGCCCTCTCTGGGGCTCTCGTGGCCCTGTCTGCGAGCTCCGCTGTGCT 60
Db 25 ATGAGCTCGCGCCCTCTCTGGGGCTCTCGTGGCCCTGTCTGCGAGCTCCGCTGTGCT 84
QY 61 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCCTGTGCTGCTGCGCTGGAGTCGGGCGG 120
Db 85 TTCTTAGTGGCTCGGCCAAGCTGTGGCCAGCCTGTGCTGCTGCGCTGGAGTCGGGCGG 144
QY 121 GAGGCCGGGCGCGGACCTGTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180
Db 145 GAGGCCGGGCGCGGACCTGTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 204
QY 181 CTGAGCAGCTGGGATCCCCCGTGAACACCTCATAGAGGGCTCCAGAAAGTGTGTGGCT 240
Db 205 CTGAGCAGCTGGGATCCCCCGTGAACACCTCATAGAGGGCTCCAGAAAGTGTGTGGCT 264
QY 241 GAGCTGGTCCCCAGGCTGGGGCCGTGAGGCCCTGAAGGCCCTGTGGGGGCCCTG 300

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Db      265 GAGCTGGGTCCCGAGCGCTGGGGCCGTGAAGCCCTGAAGCCCTGCTGCTGGGGCCCTG 324
QY      301 ACAGTGTGTGGC 312
Db      325 ACAGTGTGTGGC 336

RESULT 9
LOCUS   CB049699
DEFINITION NISC g112e05.y1 NCI CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271401
5', mRNA sequence.
ACCESSION CB049699
VERSION   CB049699.1 GI:27787986
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 437)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE     Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgaps-remain@nih.gov
          cDNA Library Preparation:
          DNA Library Arrayed by: The I.M.A.G.E. Consortium/LINL
          DNA Sequencing by: National Institutes of Health Intramural
          Sequencing Center (NISC)
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LINL at:
          info@image.lni.gov
          Plate: L1AM8008 row: J column: 10
          Seq primer: M13RP1 reverse primer (ABI).
FEATURES
    source
        1..437
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3271401"
            /sex="male"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Pr28"
            /note="Organ: prostate; Vector: pRT3D-Pac (Pharmacia)
            with a modified polylinker; Plasmid DNA from the
            normalized library NCI CGAP Pr22 was prepared, and ss
            circles were made in vitro. Following HAP purification,
            this DNA was used as tracer in a subtractive hybridization
            reaction. The driver was PCR-amplified cDNAs from a pool
            of 5,000 clones made from the same library (cloneds
            985608-986759, 1101192-1101959, and 1217928-1220615).
            Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match          97.4%; Score 303.8; DB 14; Length 437;
Best Local Similarity 99.3%; Pred. No. 1.7e-41;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GCTCGCCCTCTCTGGGCTCTGGTGGCCCTGCTGCTGCGCTGGAGTCCGGCGGGAGGC 125
Db      10 GCTCGCCCTCTCTGGGCTCTGGTGGCCCTGCTGCTGCGCTGGAGTCCGGCGGGAGGC 129
QY      66 AGTGGCTCGGCCAAGCCTGTGGCCACCCCTGCTGCTGCGCTGGAGTCCGGCGGGAGGC 125
Db      70 AGTGGCTCGGCCAAGCCTGTGGCCACCCCTGCTGCTGCGCTGGAGTCCGGCGGGAGGC 129
QY      126 CGGGCCGGGACCTGGGCAACCCCTCGGCACCCCTCAACCCGTGAAGCTCTGCTGAG 185
Db      130 CGGGCCGGGACCTGGGCAACCCCTCGGCACCCCTCAACCCGTGAAGCTCTGCTGAG 189
QY      186 CAGCTGGGCATCCCGCTGAACCCCTCATAGAGGGCTCCAGAGTGTGTGGCTGAGCT 245

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Db      190 CAGCTGGGCATCCCGCTGAACCACTCATAGAGGGCTCCAGAGTGTGTGGCTGAGCT 249
QY      246 GGGTCCCGAGCCGCTGGGGCCGTGAAGCCCTGAAGCCCTGAGCCGCTGCTGGGGCCCTGACAGT 305
Db      250 GGGTCCCGAGCCGCTGGGGCCGTGAAGCCCTGAAGCCCTGCTGGGGCCCTGACAGT 309
QY      306 GTTTGGC 312
Db      310 GTTTGGC 316

RESULT 10
LOCUS   BM977779
DEFINITION UI-CF-EN1-aef-n-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
5', mRNA sequence.
ACCESSION BM977779
VERSION   BM977779.1 GI:19596542
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 472)
REFERENCE Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    889548
COMMENT   Contact: McCray, PB
          McCray Lab
          University of Iowa
          2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
          Tel: 319 356 4866
          Fax: 319 356 7171
          Email: paul-mccray@uiowa.edu
          Tissue Procurement: Dr. M. J. Welsh, University of Iowa
          cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research
          Genetics (www.resgen.com) or from Open Biosystems
          (www.openbiosystems.com).
          Seq primer: M13 FORWARD
          POLYA=Yes
FEATURES
    source
        1..472
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="UI-CF-EN1-aef-n-17-0-UI"
            /tissue_type="Primary Lung Cystic Fibrosis Epithelial
            Cells"
            /dev_stage="Adult"
            /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
            /clone_lib="UI-CF-EN1"
            /note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a
            modified polylinker; Site 1: EcoR I; Site 2: Not I;
            UI-CF-EN1 is a normalized cDNA library containing the
            following tissue(s): Primary Lung Cystic Fibrosis
            Epithelial Cells. The library was constructed according to
            Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
            1996. First strand cDNA synthesis was primed with an
            oligo-dT primer containing a Not I site. Double stranded
            cDNA was ligated to an EcoR I adaptor, digested with Not
            I, and cloned directionally into pRT3-Pac vector. The
            oligonucleotide used to prime the synthesis of
            first-strand cDNA contains a library tag sequence that is
            located between the Not I site and the (dT)18 tail. The
            sequence tag for this library is CTGCTCAGT.
            TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS

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6hr to LPS 24h
TAG LIB=UI-CF-BN1
TAG_SEQ=CTGCTCAGGT"

Query Match 96.1%; Score 299.8; DB 12; Length 472;
Best Local Similarity 97.7%; Pred. No. 7.9e-41;
Matches 304; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ORIGIN

1 ATCAAGCTCGCCGCTCTGCTGGGCTCTGCTGGCCCTGCTGAGCTCCGCTCGTGGCT 60
|||||
458 ATGAAGCTCCCGCCCTCTGCTGGGCTTGGTGCCCTGCTGAGCTCCGCTGCTGCT 399
|||||
61 TTCTTAGTGGCTCGGCAAGCCCTGTGCTGGCCAGCTCTGCTGCTGGAGTGGGGGG 120
|||||
398 TTTTATAGTGGCTCGGCAAGCCCTGTGCTGGCCAGCTCTGCTGCTGGAGTGGGGGG 399
|||||
121 GAGGCGGGGCGGGACCTTGGCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTG 180
|||||
338 GAGGCGGGGCGGGACCTTGGCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTG 279
|||||
181 CTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 240
|||||
278 TTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 219
|||||
241 GAGCTGGTCCCCAGGCGCTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCCCTG 300
|||||
218 GAGCTGGTCCCCAGGCGCTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCCCTG 159
|||||
301 ACAGTGTGG 311
|||||
158 ACAGTGTGG 148
|||||

RESULT 11
AI685860/c
LOCUS
DEFINITION
t90f09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248841 3',
mRNA sequence.

ACCESSION
AI685860
VERSION
AI685860.1 GI:4897154
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

REFERENCE
1 (bases 1 to 439)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

Location/Qualifiers
1. .439
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2248841"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)

FEATURES
source
1. .439
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2248841"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 95.8%; Score 298.8; DB 9; Length 439;
Best Local Similarity 99.3%; Pred. No. 1.1e-40;
Matches 300; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

11 CCGCCCTCTCTGGGCTCTGCTGGCCCTGCTGAGCTCCGCTCGTGTCTTAGTGG 70
|||||
439 CCGCCCTCTCTGGGCTCTGCTGGCCCTGCTGAGCTCCGCTCGTGTCTTAGTGG 380
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71 GCTCGGCCAAGCTGTGGCCAGCTGTGCTGCTGAGTGGCGGGAGGCGGGG 130
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379 GCTCGGCCAAGCTGTGGCCAGCTGTGCTGCTGAGTGGCGGGAGGCGGGG 320
|||||
131 CCGGGACCTTGGCCACCCCTCGGCACCTCAACCCGCTGAGCTCTCTGAGCAGCC 190
|||||
319 CCGGGACCTTGGCCACCCCTCGGCACCTCAACCCGCTGAGCTCTCTGAGCAGCC 260
|||||
191 TGGGCATCCCGCTGAAACCACTCATAGAGGCTCCAGAAAGTGTGGTGAAGTCTGG 250
|||||
259 TGGGCATCCCGCTGAAACCACTCATAGAGGCTCCAGAAAGTGTGGTGAAGTCTGG 200
|||||
251 CCAGGCGCTGGGGCGGCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGACAGTGT 310
|||||
199 CCAGGCGCTGGGGCGGCTGAAGGCCCTGCTGGGGGCCCTGACAGTGT 140
|||||

311 GC 312
139 GC 138

RESULT 12
BI819045
LOCUS
DEFINITION
603033186F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174540 5',
mRNA sequence.

ACCESSION
BI819045
VERSION
BI819045.1 GI:15930595
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

REFERENCE
1 (bases 1 to 961)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM11434 row: k column: 21
High quality sequence start: 3
High quality sequence stop: 511.
Location/Qualifiers
1. .961
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5174540"

FEATURES
source
1. .961
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5174540"

/lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: Pooled brain, lung, testis; Vector:
 PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.4%; Score 297.8; DB 12; Length 961;
 Best Local Similarity 99.0%; Pred. No. 2.1e-40;
 Matches 310; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGAAGCTCGCC-GCCCTCCCTGGGGCTCTGGCTGGCCCTGTCTCAGCTCCGCTCGTGC 59
 Db 21 ATGAAGCTCGCCGCCCTCTGGGGCTCTGGCTGGCCCTGTCTCAGCTCCGCTCGTGC 80

QY 60 TTCTTATTAGGGCTCGGCCAAGCCCTGTGGCCAGCCTGTGCTGCTGCTGAGTGGCGGC 119
 Db 81 TTCTTATTAGGGCTCGGCCAAGCCCTGTGGCCAGCCTGTGCTGCTGAGTGGCGGC 140

QY 120 GGAGCGGGCGGCGGACCCCTGGCCAAAGCCCTCGGACCCCTCAACCGCTGAAGCTCCT 179
 Db 141 GGAGCGGGCGGCGGACCCCTGGCCAAAGCCCTCGGACCCCTCAACCGCTGAAGCTCCT 200

QY 180 GCTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGAGTGTGTGGC 239
 Db 201 GCTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGAGTGTGTGGC 260

QY 240 TGAGCTGGTCCCCAGGCGGCGTGAAGCCCTGAAGCCCTGTGCTGGGGCGCCT 299
 Db 261 TGAGCTGGTCCCCAGGCGGCGTGAAGCCCTGAAGCCCTGTGCTGGGGCGCCT 320

QY 300 GACAGTGTGGC 312
 Db 321 GACAGTGTGGC 333

RESULT 13
 BI820788
 LOCUS 603034390F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175502 5',
 DEFINITION mRNA sequence.
 ACCESSION BI820788
 VERSION BI820788.1 GI:15932338
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 407)
 NIH-MGC http://imgc.ncbi.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11437 row: c column: 23
 High quality sequence start: 4
 High quality sequence stop: 405.
 Location/Qualifiers
 1. .407

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11437 row: c column: 23
 High quality sequence start: 4
 High quality sequence stop: 405.
 Location/Qualifiers
 1. .407

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5175502"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: Pooled brain, lung, testis; Vector:
 PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.1%; Score 296.8; DB 12; Length 407;
 Best Local Similarity 99.0%; Pred. No. 2.4e-40;
 Matches 309; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGGCTGGCCCTGTGCTGACCTCGCTCGTGC 60
 Db 8 ATGAAGCTCGCGCCCTCTGGGGCTCTGGCTGGCCCTGTGCTGACCTCGCTCGTGC 66

QY 61 TTCTTATTAGGGCTCGGCCAAGCCCTGTGGCCAGCCTGTGCTGCTGAGTGGCGGC 120
 Db 67 TTCTTATTAGGGCTCGGCCAAGCCCTGTGGCCAGCCTGTGCTGCTGAGTGGCGGC 126

QY 121 GAGGCCGGGGCGGAGCCCTGGCCAAAGCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 180
 Db 127 GAGGCCGGGGCGGAGCCCTGGCCAAAGCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 186

QY 181 CTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
 Db 187 CTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCCAAGAGTGTGTGGCT 246

QY 241 GAGCTGGTCCCCAGGCGGCGTGAAGCCCTGAAGCCCTGTGCTGGGGCGCCTG 300
 Db 247 GAGCTGGTCCCCAGGCGGCGTGAAGCCCTGTGCTGGGGCGCCTG 306

QY 301 ACAGTGTGGC 312
 Db 307 ACAGTGTGGC 318

RESULT 14
 BI490604/c
 LOCUS 603032283T1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173268 3',
 DEFINITION mRNA sequence.
 ACCESSION BI490604
 VERSION BI490604.1 GI:15329832
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 416)
 NIH-MGC http://imgc.ncbi.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11431 row: f column: 21

High quality sequence start: 6
High quality sequence stop: 416.
Location/Qualifiers
source
1. 416

/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5173268"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.1%; Score 296.8; DB 12; Length 416;
Best Local Similarity 99.0%; Pred. No. 2.5e-40;
Matches 309; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGAAGCTGCGCCCTCTCGGGGCTCTGGTGGCCCTGTCGAGCTCCGTCGTGCT 60
DB 393 ATGAAGCTGCGCCCTCTCGGGGCTCTGGTGGCCCTGTCGAGCTCCGTCGTGCT 334

QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGCG 120
DB 333 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGCG 274

QY 121 GAGGCGGGGCGGGGACCTCGGCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180
DB 273 GAGGCGGGGCGGGGACCTCGGCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 215

QY 181 CTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 240
DB 214 CTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 155

QY 241 GAGCTGGTCCCAGGCCCTGGGGCGGTGAAGCCCTGAGGCCCTGCTGGGGGCGCTG 300
DB 154 GAGCTGGTCCCAGGCCCTGGGGCGGTGAAGGCCCTGAGGCCCTGCTGGGGGCGCTG 95

QY 301 ACAGTGTGTTGGC 312
DB 94 ACAGTGTGTTGGC 83

RESULT 15
BI819014
LOCUS
DEFINITION
603033130F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174526 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI819014 491 bp mRNA linear EST 04-OCT-2001
603033130F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174526 5',
mRNA sequence.
BI819014
BI819014.1 GI:15930564
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 491)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11434 row: k column: 07
High quality sequence stop: 470.
Location/Qualifiers
source
1. 491

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5174526"
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/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.1%; Score 296.8; DB 12; Length 491;
Best Local Similarity 99.0%; Pred. No. 2.6e-40;
Matches 309; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGAAGCTGCGCCCTCTCGGGGCTCTGGTGGCCCTGTCGAGCTCCGTCGTGCT 60
DB 22 ATGAAGCTGCGCG-CTCTCTGGGGCTCTGCGTGGCCCTGTCGAGCTCCGTCGTGCT 80

QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGCG 120
DB 81 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGCG 140

QY 121 GAGGCGGGGCGGGGACCTCGGCCAACCCTCGGCACCCCTCAACCCGCTGAAGTCTCTG 180
DB 141 GAGGCGGGGCGGGGACCTCGGCCAACCCTCGGCACCCCTCAACCCGCTGAAGTCTCTG 200

QY 181 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 240
DB 201 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 260

QY 241 GAGCTGGTCCCAGGCCCTGGGGCGGTGAAGGCCCTGTAAGGCCCTGCTGGGGGCGCTG 300
DB 261 GAGCTGGTCCCAGGCCCTGGGGCGGTGAAGGCCCTGTAAGGCCCTGCTGGGGGCGCTG 320

QY 301 ACAGTGTGTTGGC 312
DB 321 ACAGTGTGTTGGC 332

Search completed: June 6, 2004, 15:41:35
Job time : 2503 secs

Alt	Score	Query Match	Length	DB	ID	Description
1	56.4	18.1	263	2	US-08-964-725-2	Sequence 2, Appli
2	56.4	18.1	507	2	US-08-964-725-4	Sequence 4, Appli
3	56.4	18.1	519	2	US-08-964-725-5	Sequence 5, Appli
4	52.4	16.8	509	4	US-09-023-655-267	Sequence 267, App
5	49.2	15.8	2497	4	US-09-620-1320-47	Sequence 47, Appl
6	46.6	14.9	2274	4	US-09-252-991A-3660	Sequence 3660, Ap
7	46.6	14.9	3297	4	US-09-252-991A-3616	Sequence 3615, Ap
8	46.2	14.8	432	4	US-09-252-991A-13281	Sequence 13281, A
9	46.2	14.8	1425	4	US-09-252-991A-12820	Sequence 12820, A
10	46.2	14.8	1428	4	US-09-252-991A-12677	Sequence 12677, A
11	46.2	14.8	1611	4	US-09-252-991A-13122	Sequence 13122, A
12	44.2	14.2	729	4	US-09-252-991A-7316	Sequence 7316, Ap
13	44.2	14.2	1083	4	US-09-252-991A-7185	Sequence 7185, Ap
14	44.2	14.2	1572	4	US-09-252-991A-7304	Sequence 7304, Ap
15	44.2	14.2	2543	1	US-08-555-669-11	Sequence 11, Appl
16	44.2	14.2	2543	3	US-09-073-663-11	Sequence 11, Appl
17	44.2	14.2	2574	4	US-09-252-991A-7385	Sequence 7385, Ap
18	43.6	14.0	432	1	US-08-642-255-48	Sequence 48, Appl
19	43.6	14.0	756	1	US-08-642-255-50	Sequence 50, Appl
20	42.6	13.7	2721	6	5215881-2	Patent No. 5215881
21	42.6	13.7	8438	1	US-07-945-283-1	Sequence 1, Appli
22	42.2	13.5	930	4	US-09-252-991A-1173	Sequence 1173, Ap
23	42.2	13.5	1116	4	US-09-252-991A-8338	Sequence 8238, Ap
24	42.2	13.5	1122	4	US-09-252-991A-7974	Sequence 7974, Ap
25	42.2	13.5	1125	4	US-09-252-991A-8074	Sequence 8074, Ap
26	42.2	13.5	1836	4	US-09-475-515-47	Sequence 47, Appl
27	42.2	13.5	1944	4	US-09-475-515-37	Sequence 37, Appl

US-08-964-725-2

Query Match 18.1%; Score 56.4; DB 2; Length 263;
Best Local Similarity 60.4%; Pred. No. 0.0013;
Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 137 CCTGGGCAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTCTGAGAGCCTGGGCA 196
DB 60 CTCGGACAACAATCTCCCTTTAAGATCCATTAAAGCTTCTTCTGAAAACTCTGGCA 119
QY 197 TCCCGGTGAACCACTCATAGAGGGCTCCAGAAAGTGTGTGGCTGAGCTGGGTCCCAAG 256
DB 120 TTTCTGTGAGCACCTTGTGGAGGGCTAAGAAAGTGTGTAATGAGCTGGGACCAAGG 179
QY 257 CCGTGGGGCGGTGAAGCCCTGAAGCCCTGCT 290
DB 180 CTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCT 213

RESULT 2

US-08-964-725-4
; Sequence 4, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 18.1%; Score 56.4; DB 2; Length 507;
Best Local Similarity 60.4%; Pred. No. 0.0014;

Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 137 CCTGGGCAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTCTGAGAGCCTGGGCA 196
DB 195 CTCGGACAACAATCTCTCCCTTTATGATCCATTAAAGCTTCTTCTGAAAACTCTGGCA 254
QY 197 TCCCGGTGAACCACTCATAGAGGGCTCCAGAAAGTGTGTGGCTGAGCTGGGTCCCAAG 256
DB 255 TTTCTGTGAGCACCTTGTGGAGGGCTAAGAAAGTGTGTAATGAGCTGGGACCAAGG 314
QY 257 CCGTGGGGCGGTGAAGCCCTGAAGCCCTGCT 290
DB 315 CTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCT 348

RESULT 3

US-08-964-725-5
; Sequence 5, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 18.1%; Score 56.4; DB 2; Length 519;
Best Local Similarity 60.4%; Pred. No. 0.0014;

Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 137 CCTGGGCAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTCTGAGAGCCTGGGCA 196

Db 208 CTCTGGACAACTCTTCCTTTATGTATCCATTAAAGCTTCTTCTGAAACTCTGGGCA 267
QY 197 TCCCGTGAACCACTATAGAGGCTCCAGAGTGTGTGGCTAGCTGGGTCCCGAGG 256
Db 268 TTTCGTTGAGCACCTTGTGGAGGCTTAGAGAGTGTGTAATAGCTGGGACCGAGG 327
QY 257 CGGTGGGGCCGTGAAGGCCCTTGAAGGCCCTGCT 290
Db 328 CTCTGAAGCTGTGAAGAACTGCTGGAGGCGCT 361

RESULT 4

US-09-023-655-267
; Sequence 267, Application US/03023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT01
; CLONE: 126758
US-09-023-655-267
Query Match 16.8%; Score 52.4; DB 4; Length 509;
Best Local Similarity 59.3%; Pred. No. 0.0092;
Matches 89; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 141 GGCACACCCCTCGGCACCTCAACCCGCTGAAGCTCTCTGAGCAGGCTGGGATCCC 200
Db 201 GACAAACATCTCTCCCTTTATGGATCCATTAAAGCTTCTTCTGAAACTCTGGGCAATTTC 260
QY 201 CGTGAACCACTCATAGAGGCTCCAGAGTGTGTGGCTGAGCTGGTGGTCCCGAGGCCCT 260
Db 261 TGTGAGCACTTGTGGAGGGCTTAGAGAGTGTGTAATAGCTGGGACCGAGGCTTC 320
QY 261 GGGGGCGTGAAGGCCCTGAAGGCCCTGCT 290

Db 321 TGAAGCTGTGAAGAACTGCTGGAGGCGCT 350

RESULT 5

US-09-620-312D-47
; Sequence 47, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chinghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 47
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(1756)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2497)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-47

Query Match 15.8%; Score 49.2; DB 4; Length 2497;
Best Local Similarity 50.0%; Pred. No. 0.045;
Matches 151; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
QY 3 GAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTGCTGACGCTCGCTCGTCTGCTTT 62
Db 1099 GTACCTGGTCCCTGAGCGGCGCTGAGGAGCTTGGGACAGTCCCTCGCGGCTT 1158
QY 63 CTTAGTGGGCTG---GCCAAGCTGTGGCCAGCCTGTGCTGGCTGGAGTGGGCGGC 119
Db 1159 CTTGGGGAGGTGGGTGCTCCGCTCTGCGGCGCCCGGGGGGCGCTCGTGGGCGCGC 1218
QY 120 GGAGCGCGGCGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCT 179
Db 1219 TCGGCCATGGGTGGGCGCTGGGTCCATGCTGGGCTCATGACTACGGGCGCGCA 1278
QY 180 GGTGAGCAGCTTGGCATCCCGTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGC 239
Db 1279 ATTCCAGTCCCTGGACAGCATGCGGCGCTGATCCGCGCTTCCCGAGGCTTCGCG 1338
QY 240 TGAGCTGGTCCCGAGGCGCGTGGGGCGCTGAAGGCCCTGTGTTGGGGCGCT 299
Db 1339 CAAGCTAACCACTGTGTGGATGCCAGCGCGGCGCTTTCACCGCTTACCTGGAAGCAAT 1398

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Qy 300 GA 301
Db 1399 GA 1400

Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 88 GCCAGCCTGTCCTCGGTGGTGGAGTCGGCGCGGAGGCGCGGCGGACCTTGGCCAAAC 147
Db 161 GTCCTGGTTTCCCGCGGCGAGCGCTCGCGCGCGAGATCCGACCCGATACCCGCCAGTAC 220

Qy 148 CCCTCGGCACCTCAACCGCTGAAGCTCCTCTGAGCAGCCTGGGCATCCCGTGAAC 207
Db 221 TACGGCTGCCCGCGAGCGCTGGAGAGCGCTGAACACCTAGGCCCGCAGCGCGC 280

Qy 208 CACCTCATAGAGGGCTCCCAAGAGTGTGTGGCTGAGCTGGGTCCCGAGGCGGTGGGGGCC 267
Db 281 GTGCTGATCCCTTCAGCCCGGAGACAGACCGCGCGCGGCGAGCCAGCGGTGGACGGC 340

Qy 268 GTGAAGGCCCTGAAGCCCTGTGGGGCCCTG 300
Db 341 GAGTACACCTGGAGGAAGCCCTGGCGCCCTG 373

RESULT 8
US-09-252-991A-13281/c
; Sequence 13281, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13281
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13281

Query Match 14.8%; Score 46.2; DB 4; Length 432;
Best Local Similarity 47.2%; Pred. No. 0.18;
Matches 141; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy 9 CGCGCCCTCTCGGGGCTCTGGTGGCCCTGTCTGAGCTCCGCTCGTCTTCTTAGT 68
Db 408 CGCGGTGGGACCGGGCTCAACGCGCGGAGGGCTTCGCGAGCCATCCCGCGGAAT 349

Qy 69 GGGCTCGGCCCAAGCCTGTGGCCAGCCTGTCTGAGTGGCGCGGAGGCGCGG 128
Db 348 CGCGCGGATCGGGCTGTCTGCGCGGCGGAGCAAGTTCGCCGCCCTGGCGCG 289

Qy 129 GGCGGGACCTTGGCCAAACCCCTCGGCAACCTCAACCCGCTGAGCTCTGCTGAGCAG 188
Db 288 CCAGAGCGCTGTGTCATCTCTCGCGCGCCCTGAAGAGCTTCGCGGTGGCCCTGATGA 229

Qy 189 CCTGGGATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGTGCTGAGCTGGG 248
Db 228 GATCGCAACGACCTGCGCTGTCTCGGTCGCGCGCGGCTTCGCCCGAGGTGA 169

Qy 249 TCCCGAGGCGGTGGGGCCGCTGAAGGCCCTGAAGGCCCTGAGGGGCCCTGACAGTGT 307
Db 168 GCTCGCGCCCAACGAGCGCGGCGCTCGATCATGCTCCCGGCAAGTCAACCCGACGT 110

RESULT 9
US-09-252-991A-12820
; Sequence 12820, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```


;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 12820

;; LENGTH: 1425

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-12820

Query Match 14.8%; Score 46.2; DB 4; Length 1425;

Best Local Similarity 47.2%; Pred. No. 0.18; Indels 0; Gaps 0;

Matches 141; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CGCCGCGCTCTCGGGGCTCTGGGTGGCCCTGCTCTGCAGCTCGGCTCGTCTTCTTAGT 68

DB 714 CGCGGTGGCCACCGGGCTCAACGCGCGGAAGGCTTCGCCGAGCCATCGCCGCGGAAT 773

QY 69 GGGCTCGCCCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTCGGCGGGAGGCGCG 128

DB 774 CGCCGCGGAATCGGGCTCGCTTCGTCGCGCGCGCAAGTTCCGCGCCCTGGCGCG 833

QY 129 GCGCGGACCTTGGCAACCCCTCGGCACTCTCAACCCGCTGAAGCTCTCTGAGCAG 188

DB 834 CCACGAGCGCTGGTTCATCTCTCCGCGCCCTGGAAGCGCTGGCGGTGGCCCTGATGA 993

QY 189 CCTGGGCATCCCGTGAACCACTCTATAGAGGCTCCAGAGTGTGTGGCTGAGCTGGG 248

DB 894 GATGCCAAGACCTTGGCTGTCTCGGTTCCGCGCCACGCGCGGCTTCGCCGAGTGA 953

QY 249 TCCCGCAGCGTGGGGCGCTGAAGCCCTGAAGCCCTGCTGGGGGCGCTGACATGT 307

DB 954 GCTGCGCGCAACGACGCGGAGCTCGATCATGTGCGCGCAAGTCAACCCGACCCAGT 1012

RESULT 10

US-09-252-991A-12677

;; Sequence 12677, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 12677

;; LENGTH: 1428

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-12677

Query Match 14.8%; Score 46.2; DB 4; Length 1428;

Best Local Similarity 47.2%; Pred. No. 0.18;

Matches 141; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CGCCGCGCTCTCGGGGCTCTGGGTGGCCCTGCTCTGCAGCTCGGCTCGTCTTCTTAGT 68

DB 561 CGCGGTGGCCACCGGGCTCAACGCGCGGAAGGCTTCGCCGAGCCATCGCCGCGGAAT 720

QY 69 GGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTCGGCGGGAGGCGCG 128

DB 721 CGCCGCGGAATCGGGCTCGCTTCGTCGCGCGCGCAAGTTCGCGGCCCTCGCGCG 780

QY 129 GCGCGGACCTTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTCTGAGCAG 188

DB 781 CCACGAGCGCTGGTTCATCTCTCGCGCGCCCTGAAGAGCCCTGGCGGCTGATGAA 840

QY 189 CTGGGCTATCCCGTGAACCACTCTATAGAGGCTCCAGAAAGTGTGTGGCTGAGCTGG 248

DB 841 GATCGCCAAACGACCTTGGCGCTTCTCGGTTCCGCGCCACGCGCGCTTGGCGAGGTGA 900

QY 249 TCCCGCAGCGCTGGGGCGCTGAAGCCCTGAAGCCCTGCTGGGGGCGCTGACAGTGT 307

DB 901 GCTCGCGCCAAACGAGCGCGGCGAGCTCGATCATGCTCCGCGAAGTCAACCCGACCCAGT 959

RESULT 11

US-09-252-991A-13122/c

;; Sequence 13122, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 13122

;; LENGTH: 1611

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-13122

Query Match 14.8%; Score 46.2; DB 4; Length 1611;

Best Local Similarity 47.2%; Pred. No. 0.19;

Matches 141; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CGCCGCGCTCTCGGGGCTCTGGGTGGCCCTGCTCTGCAGCTCGGCTCGTCTTCTTAGT 68

DB 817 CGCGGTGGGACCGGGGCTCAACGCGCGGAAGGCTTCGCCGAGCCATCGCCGCGGAAT 758

QY 69 GGGCTCGGCCAAGCCTGTGGCCAGCCTGTCTCGCTGGAGTCGGCGGGAGGCGCG 128

DB 757 CGCCCGCGAATCGGGCTGCTTCTGTCGCGCGCGCAAGTTCGCGCGCTGGCGCG 698

QY 129 GCGCGGACCTTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTCTGCTGAGCAG 188

DB 697 CCACGAGCGCTGGTTCATCTCTCGCGCGCCCTGAAGAGCTTGGCGGCTGATGAA 638

QY 189 CTGGGCTATCCCGTGAACCACTCTATAGAGGCTCCAGAAAGTGTGTGCTGAGCTGG 248

DB 637 GATCGCCAAACGACCTTGGCGCTCTCGGTTCCGCGCCACGCGCGCTTGGCGAGGTGA 578

QY 249 TCCCGCAGCGCTGGGGCGCTGAAGCCCTGAAGCCCTGCTGGGGGCGCTGACAGTGT 307

DB 577 GCTCGCGCCAAACGAGCGCGGCGAGCTCGATCATGCTCCGCGAAGTCAACCCGACCCAGT 519

RESULT 12

US-09-252-991A-7316

;; Sequence 7316, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788


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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7316
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7316

Query Match
Best Local Similarity 14.2%; Score 44.2; DB 4; Length 729;
Matches 131; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 26 TCTGCGTGGCCCTGCTCTGAGCTCCGCTCGTGTCTTCTTAGTGGCTCGGCCAAGCCTG 85
Db 240 TCGAGGCGGCGCGCGCCGACCAAGGTCGAGGCTTCGCGTGTGTCGCCGACGAGGTGC 299
QY 86 TGGCCACGCTGTGCTCGGCTGGAGTGGCGGGGAGGCGGGCGGGGACCCCTGGGCCA 145
Db 300 GGGGCTGGCGCGCGCCACCAACAGTCCACGGCGGAGATCGAGACCCCTGATCGGTGCT 359
QY 146 ACCGCTCGGACCCCTCAACCGCTGAACTCCTGCTGAGCAGCTGGGATCCCGCTGA 205
Db 360 TGCAGATGGACGAGCAGGCGGTGACGCTATGACGCGAGCCACCAAGTTG---GTGG 416
QY 206 ACCACCTCATAGAGGGCTCCAGAAAGTGTGTGGTGTAGCTGGTCCCGCGGCTGGGGG 265
Db 417 ACCAGGCGTGCAGACGCTTTCAGACCGAGGCGGCGCTGGGCAACATCCGCGCGG 476
QY 266 CCGTGAAGGCCCTGAAG 282
Db 477 TGGCGCTGATCCAGCAG 493

RESULT 13
US-09-252-991A-7185/c
; Sequence 7185, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7185
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7185

Query Match
Best Local Similarity 14.2%; Score 44.2; DB 4; Length 1083;
Matches 131; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 26 TCTGCGTGGCCCTGCTCTGAGCTCCGCTCGTGTCTTCTTAGTGGCTCGGCCAAGCCTG 85
Db 346 TCGAGGCGGCGCGCGCCGACCAAGGTCGAGGCTTCGCGTGTGTCGCCGACGAGGTGC 287
QY 86 TGGCCACGCTGTGCTCGGCTGGAGTGGCGGGGAGGCGGGCGGGGACCCCTGGGCCA 145
Db 286 GGGGCTGGCGCGCGCCACCAACAGTCCACGGCGGAGATCGAGACCCCTGATCGGTGCT 227
QY 146 ACCGCTCGGACCCCTCAACCGCTGAACTCCTGCTGAGCAGCTGGGATCCCGCTGA 205
Db 226 TGCAGATGGACGAGCAGGCGGTGACGCTATGACGCGGAGCCACCAAGTTG---GTGG 170

RESULT 14
US-09-252-991A-7304/c
; Sequence 7304, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7304
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7304

Query Match
Best Local Similarity 14.2%; Score 44.2; DB 4; Length 1572;
Matches 131; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 26 TCTGCGTGGCCCTGCTCTGAGCTCCGCTCGTGTCTTCTTAGTGGCTCGGCCAAGCCTG 85
Db 413 TCGAGGCGGCGCGCGCCGACCAAGGTCGAGGCTTCGCGTGTGTCGCCGACGAGGTGC 354
QY 86 TGGCCACGCTGTGCTCGGCTGGAGTGGCGGGGAGGCGGGCGGGGACCCCTGGGCCA 145
Db 353 GGGGCTGGCGCGCGCCACCAACAGTCCACGGCGGAGATCGAGACCCCTGATCGGTGCT 294
QY 146 ACCGCTCGGACCCCTCAACCGCTGAACTCCTGCTGAGCAGCTGGGATCCCGCTGA 205
Db 293 TGCAGATGGACGAGCAGGCGGTGACGCTATGACGCGAGCCACCAAGTTG---GTGG 237
QY 206 ACCACCTCATAGAGGGCTCCAGAAAGTGTGTGGTGTAGCTGGTCCCGCGGCTGGGGG 265
Db 236 ACCAGAGCGTCGACGAGCGGCTTCAGACCGAGGCGGCTGGGCAACATCGCCACGCGG 177
QY 266 CCGTGAAGGCCCTGAAG 282
Db 176 TGGCGCTGATCCAGCAG 160

RESULT 15
US-08-555-669-11
; Sequence 11, Application US/08555669
; Patent No. 5773248
; GENERAL INFORMATION:
; APPLICANT: Brewton, Richard G.
; APPLICANT: Mayne, Richard
; TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,669
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 47..2098
US-08-555-669-11

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Query Match	14.2%;	Score 44.2;	DB 1;	Length 2543;
Best Local Similarity	47.3%;	Pred. No. 0.49;		
Matches 133;	Conservative 0;	Mismatches 148;	Indels 0;	Gaps 0;
QY	6	GCTCGCGCGCCCTCTGGGCGCTGCGCTGGCCCTGTCTCTGCAGCTTCGCTCGCTGCTTCTT	65	
Dbb	1211	GGCCTCGGCCCAAGAGGCCCTCCCGAGGCCCTGGTGTCCGAGGCTTCCAGGCGCCAGAAG	1270	
QY	66	AGTGGGCTCGGCCAAGCCTGTGSCCCAGACCTGTGCTGCGCTCGCTGAGCTCGCGCGCGGAGGC	125	
Dbb	1271	GGCAGCATGGGAGACCCCGGCCCTTCCAGGCCCCCGAGGCCCTCGAGGTGACGTGGCGCAC	1330	
QY	126	CGGGGCGGGACCCCTGGGCCAACCCCTTCGGCACCCCTCAACCCGCTGAAGCTCTCTGCTGAG	185	
Dbb	1331	CGGGGTCCGGGAGGTGCCAAGGCCCTTAAGGAGACAGGGTATTGCAGTTCCGACGCT	1390	
QY	186	CAGCCTGGGCATCCCGTGAACCAACCTCATAGAGGCTCCCGAAGTGTGTGCTGAGCT	245	
Dbb	1391	CTTCTCTGGGATAAAGGAACTGGGTCCAGCGCCTGGTCGGACCCCAAGAGGAGTCT	1450	
QY	246	GGGTCCCAAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCC	286	
Dbb	1451	GGCAGTCTGAGGGGAGCTGGGCCCCCAAGGACCCAGGGTCC	1491	

Search completed: June 6, 2004, 15:43:07
Job time : 81 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 14:59:47 ; Search time 326 Seconds
(without alignments)

4366.082 Million cell updates/sec

Title: US-10-081-817A-3

Perfect score: 312

Sequence: 1 atgaagctgcgcgcctctct.....gggcccctgacagtgttggc 312

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	308.8	99.0	569	13	US-10-211-858-27
5	308.8	99.0	569	15	US-10-210-951-27
6	308.8	99.0	569	15	US-10-211-884-27
7	308.8	99.0	570	9	US-09-989-722-407
8	308.8	99.0	570	9	US-09-989-723-407
9	308.8	99.0	570	9	US-09-989-727-407
10	308.8	99.0	570	9	US-09-989-727-407
11	308.8	99.0	570	9	US-09-989-731-407
12	308.8	99.0	570	9	US-09-989-732-407
13	308.8	99.0	570	9	US-09-991-073-407
14	308.8	99.0	570	9	US-09-990-442-407

15	308.8	99.0	570	9	US-09-991-163-407	Sequence 407, App
16	308.8	99.0	570	9	US-09-993-604-407	Sequence 407, App
17	308.8	99.0	570	9	US-09-990-456-407	Sequence 407, App
18	308.8	99.0	570	9	US-09-989-721-407	Sequence 407, App
19	308.8	99.0	570	9	US-09-992-598-407	Sequence 407, App
20	308.8	99.0	570	9	US-09-989-293A-407	Sequence 407, App
21	308.8	99.0	570	9	US-09-989-735-407	Sequence 407, App
22	308.8	99.0	570	9	US-09-990-444-407	Sequence 407, App
23	308.8	99.0	570	9	US-09-991-181-407	Sequence 407, App
24	308.8	99.0	570	9	US-09-989-730-407	Sequence 407, App
25	308.8	99.0	570	9	US-09-990-436-407	Sequence 407, App
26	308.8	99.0	570	9	US-09-993-687-407	Sequence 407, App
27	308.8	99.0	570	10	US-09-989-734-407	Sequence 407, App
28	308.8	99.0	570	10	US-09-997-653-407	Sequence 407, App
29	308.8	99.0	570	10	US-09-993-667-407	Sequence 407, App
30	308.8	99.0	570	10	US-09-997-428-407	Sequence 407, App
31	308.8	99.0	570	10	US-09-997-666-407	Sequence 407, App
32	308.8	99.0	570	10	US-09-990-438-407	Sequence 407, App
33	308.8	99.0	570	10	US-09-990-562-407	Sequence 407, App
34	308.8	99.0	570	10	US-09-990-711-407	Sequence 407, App
35	308.8	99.0	570	10	US-09-988-726-407	Sequence 407, App
36	308.8	99.0	570	10	US-09-998-156-407	Sequence 407, App
37	308.8	99.0	570	10	US-09-990-437-407	Sequence 407, App
38	308.8	99.0	570	10	US-09-991-157-407	Sequence 407, App
39	308.8	99.0	570	10	US-09-997-514-407	Sequence 407, App
40	308.8	99.0	570	10	US-09-997-573-407	Sequence 407, App
41	308.8	99.0	570	10	US-09-991-172-407	Sequence 407, App
42	308.8	99.0	570	10	US-09-990-726-407	Sequence 407, App
43	308.8	99.0	570	10	US-09-997-559-407	Sequence 407, App
44	308.8	99.0	570	10	US-09-997-601-407	Sequence 407, App
45	308.8	99.0	570	10	US-09-990-443-407	Sequence 407, App

ALIGNMENTS

RESULT 1

US-10-081-817-3
; Sequence 3, Application US/10081817
; Publication No. US20020183501A1
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Porter, Dale
; APPLICANT: Sgroi, Dennis
; APPLICANT: Krop, Ian
; TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
; FILE REFERENCE: 00530-094001
; CURRENT APPLICATION NUMBER: US/10/081,817
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/270,973
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/351,908
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-081-817-3

Query Match 100.0%; Score 312; DB 14; Length 312;
Best Local Similarity 100.0%; Pred. No. 8.2e-69;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGTGGCCCTGCTGAGTCCGCTCGTCT 60
Db 1 ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGTGGCCCTGCTGAGTCCGCTCGTCT 60
QY 61 TTCTTAGTGGCTCGGCCAAGCCTGTGCGCCAGCCTGTGCGTGGAGTCGCGCGCG 120
Db 61 TTCTTAGTGGCTCGGCCAAGCCTGTGCGCCAGCCTGTGCGTGGAGTCGCGCGCG 120

Qy	121	GAGCCGGGGCGGGAACCTTGGCAACCCCTCGGCAACCTTCAACCCCGTGAAGTCTCTG	180
Db	121	GAGCCGGGGCGGGAACCTTGGCAACCCCTCGGCAACCTTCAACCCCGTGAAGTCTCTG	180
Qy	181	CTGAGCAGCCTGGGCATCCCGTGAAACCACTCATAGAGGGGTCCCAAGTGTGTGGCT	240
Db	181	CTGAGCAGCCTGGGCATCCCGTGAAACCACTCATAGAGGGGTCCCAAGTGTGTGGCT	240
Qy	241	GAGCTGGTCCCCAGCGCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGTCTGGGGGCCCTG	300
Db	241	GAGCTGGTCCCCAGCGCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGTCTGGGGGCCCTG	300
Qy	301	ACAGTGTGGC	312
Db	301	ACAGTGTGGC	312

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RESULT 2
US-10-426-002-18
; Sequence 18, Application US/10426002
; Publication No. US20040101876A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanging
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; APPLICANT: Rotem Sorkk
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 26083
; CURRENT APPLICATION NUMBER: US/10/426,002
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-002-18

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RESULT 3
US-10-237-435-6
; Sequence 6, Application US/10237435
; Publication No. US20030124580A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Spiro, Peter A.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: LONG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 US
; CURRENT APPLICATION NUMBER: US/10/237,435
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,822
; PRIOR FILING DATE: 09-07-2001
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20030124580A1 242745.1
US-10-237-435-6

Query Match          99.0%; Score 308.8; DB 15; Length 561;
Best Local Similarity 99.4%; Pred. No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 ATGAAGCTCGCCGCCCTCTGGGCTTGCGTGGCCCTCTCTGAGCTCCGCTCGTGTCT 60
Db 117 ATGAAGCTCGCGCCCTCTGGGCTCTGCGTGGCCCTCTCTGAGCTCCGCTCGTGTCT 176

QY 61 TTCTTAGTGGCTCGGCCAGACCTTGCCCAAGCTGTGCGTGGCTGGCTGAGTCCGCGGCG 120
Db 177 TTCTTAGTGGCTCGGCCAGACCTTGCCCAAGCTGTGCGTGGCTGGCTGAGTCCGCGGCG 236

QY 121 GAGCCGGGCGCGGACCCCTGGCCAAACCCCTCGGCACCCCTCAACCCCGCTGAAGCTCCTG 180
Db 237 GAGCCGGGCGCGGACCCCTGGCCAAACCCCTCGGCACCCCTCAACCCCGCTGAAGCTCCTG 296

QY 181 CTGAGCAGCTGGGCATCCCGTGAAACCACTCATAGAGGCTCCAGAGTGTGTGCT 240
Db 297 CTGAGCAGCTGGGCATCCCGTGAAACCACTCATAGAGGCTCCAGAGTGTGTGCT 356

QY 241 GAGCTGGGTCCCAAGGCGCTGGGGGCGCTGAAGGCGCTGTGAAGGCGCTGTGAAGGCGCTGT 300
Db 357 GAGCTGGGTCCCAAGGCGCTGGGGGCGCTGTGAAGGCGCTGTGAAGGCGCTGTGAAGGCGCTGT 416

QY 301 ACAGTGTGTGGC 312
Db 417 ACAGTGTGTGGC 428

RESULT 4
US-10-211-858-27
; Sequence 27, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watarabe, Colin K.

```

APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 27
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-858-27

Query Match 99.0%; Score 308.8; DB 13; Length 569;
Best Local Similarity 99.4%; Pred. No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60
Db 79 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 138
QY 61 TTCTTAGTGGCTCGGCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTCGGCGCG 120
Db 139 TTCTTAGTGGCTCGGCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTCGGCGCG 198
QY 121 GAGCGCGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCGCGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 258
QY 181 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGCTGTGGCT 240
Db 259 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGCTGTGGCT 318
QY 241 GAGCTGGTCCCGAGGCGCTGGGGCCGTGAAGCCCTGAAGCCCTGTGGGGCCCTG 300
Db 319 GAGCTGGTCCCGAGGCGCTGGGGCCGTGAAGCCCTGAAGCCCTGTGGGGCCCTG 378
QY 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390

RESULT 5
US-10-210-951-27
; Sequence 27, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.

APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/210,951
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 27
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-951-27

Query Match 99.0%; Score 308.8; DB 15; Length 569;
Best Local Similarity 99.4%; Pred. No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60
Db 79 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 138
QY 61 TTCTTAGTGGCTCGGCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTCGGCGCG 120
Db 139 TTCTTAGTGGCTCGGCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTCGGCGCG 198
QY 121 GAGCGCGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCGCGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 258
QY 181 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGCTGTGGCT 240
Db 259 CTGAGCAGCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGCTGTGGCT 318
QY 241 GAGCTGGTCCCGAGGCGCTGGGGCCGTGAAGCCCTGAAGCCCTGTGGGGCCCTG 300
Db 319 GAGCTGGTCCCGAGGCGCTGGGGCCGTGAAGCCCTGAAGCCCTGTGGGGCCCTG 378
QY 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390

RESULT 6
US-10-211-884-27
; Sequence 27, Application US/10211884
; Publication No. US20030175900A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scott A.
APPLICANT: Pan, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 27
LENGTH: 569
TYPE: DNA
ORGANISM: Homo sapiens
US-10-211-884-27
Query Match 99.0%; Score 308.8; DB 15; Length 569;
Best Local Similarity 99.4%; Pred. No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGTGGCCCTGTCTCGAGCTCCGCTCGTGC 60
DB 79 ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGTGGCCCTGTCTCGAGCTCCGCTCGTGC 138
QY 61 TTCCTAGTGGGCTCGGCAAGCTGTGGCCAGCTGTGCTGCGTGGCTGAGTGGCGCG 120
DB 139 TTCCTAGTGGGCTCGGCAAGCTGTGGCCAGCTGTGCTGCGTGGCTGAGTGGCGCG 198
QY 121 GAGGCGGGGCGGACCTCTGSCCAACCCCTCGGCACCTCAACCCCTGAAGCTCGT 180
DB 199 GAGGCGGGGCGGACCTCTGSCCAACCCCTCGGCACCTCAACCCCTGAAGCTCGT 258
QY 181 CTGAGCAGCTGGGCATCCCGTGAACCACTCAATAGAGGCTCCAGAGTGTGTGCT 240
DB 259 CTGAGCAGCTGGGCATCCCGTGAACCACTCAATAGAGGCTCCAGAGTGTGTGCT 318
QY 241 GAGCTGGTCCCGAGCGCTGGGGCCCTGAAGCCCTGAAGCCCTGAGGGGCCCTG 300
DB 319 GAGCTGGTCCCGAGCGCTGGGGCCCTGAAGCCCTGAAGCCCTGAGGGGCCCTG 378
QY 301 ACAGTGTGTC 312
DB 379 ACAGTGTGTC 390

RESULT 7
US-09-989-722-407
Sequence 407, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

;; PRIOR APPLICATION NUMBER: 60/088030
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;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 308.8; DB 9; Length 570;

Best Local Similarity 99.4%; Pred. No. 4.6e-67;

Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGGCCCTGTGGCCAGCCTGTGGCTGCGCTGCGCTGAGTTCGGCGGG	60
Db	79	ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGGCCCTGTGGCCAGCCTGTGGCTGCGCTGAGTTCGGCGGG	138
QY	61	TTCTTAGTGGGCTCGGCCCAAGCCTGTGGCCAGCCTGTGGCTGCGCTGCGCTGAGTTCGGCGGG	120
Db	139	TTCTTAGTGGGCTCGGCCCAAGCCTGTGGCCAGCCTGTGGCTGCGCTGAGTTCGGCGGG	198
QY	121	GAGGCGGGGCGGAGACCTGCGCAACCCCTCGGCACCCCTCAACCCGCTGAAGTCTCTG	180
Db	199	GAGGCGGGGCGGAGACCTGCGCAACCCCTCGGCACCCCTCAACCCGCTGAAGTCTCTG	258

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Query Match 99.0%; Score 308.8; DB 9; Length 570;

Best Local Similarity 99.4%; Pred. No. 4.6e-67;

Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCAAGCTCCCGCCCTCTGGGCTCTGGTGGCCCTCTGCTGAGCTCTGCTGAGCTCGCTCGTGGCT 60

Db 79 ATGAAGCTCCCGCCCTCTGGGCTCTGGTGGCCCTCTGCTGAGCTCTGCTGAGCTCGCTCGTGGCT 138

QY 61 TTCTTAGTGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCTGAGCTCTGCTGAGCTCGGCGGCG 120

Db 139 TTCTTAGTGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCTGAGCTCTGCTGAGCTCGGCGGCG 198

QY 121 GAGCCCGGCGCGGACCTTGGCCAAACCCCTCGGCAACCTTCAACCCCTGAGCTCTGCTG 180

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QY 181 CTGAGCAGCCTGGGCATCCCGTGAACCACTCATAGAGGCTCCCAAGAGTGTGCTGGCT 240

Db 259 CTGAGCAGCCTGGGCATCCCGTGAACCACTCATAGAGGCTCCCAAGAGTGTGCTGGCT 318

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Db 319 GAGTGGTGGTGGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTG 378

QY 301 ACAGTGTGGC 312

Db 379 ACAGTGTGGC 390

RESULT 10

US-09-989-727-407

Sequence 407, Application US/09989727

Patent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C65

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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC70
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;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 308.8; DB 9; Length 570;
Best Local Similarity 99.4%; Pred. No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 79 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGAGCTCGCTGCTGCT 138

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Db 199 GAGCGCGCGCGCGGACCTGTGCGCAACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCCTG 258

Qy 181 CTGACAGCTGGGATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGCTGCT 240
Db 259 CTGACAGCTGGGATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGCTGCTGCT 318

Qy 241 GAGCTGGTCCCGAGCGTGGGCGCGTGAAGGCCCTGAAGGCCCTGCTGGGGCCCTG 300
Db 319 GAGCTGGTCCCGAGCGTGGGCGCGTGAAGGCCCTGAAGGCCCTGCTGGGGCCCTG 378

Qy 301 ACAGTGTGTTGGC 312
Db 379 ACAGTGTGTTGGC 390

RESULT 12
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; Sequence 407, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas P.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730F1C57
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/	PRIOR FILING DATE:	1998-07-02
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/	PRIOR FILING DATE:	1998-07-07
/	PRIOR APPLICATION NUMBER:	60/091982
/	PRIOR FILING DATE:	1998-07-07
/	PRIOR APPLICATION NUMBER:	60/092182
/	PRIOR FILING DATE:	1998-07-09
/	Query Match	99.0%; Score 308.; DB 9; Length 570;
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Dd	79	ATGAAGCTCGGCCGCCCTCCTTGGGGCTCTGGGTGGCCCTGTCTCTGCAGCTCCGCTGCTGCT 138
QY	61	TTCATTAGTGGGCTCGGCCAAGACTGTGGCCCCCAACCCTCGGCACCTCAAACCCGCTGAAGCTCCGTG 120
Dd	139	TTCATTAGTGGGCTCGGCCAAGACTGTGGCCCCCACCCCTCGGCACCTCAAACCCGCTGAAGCTCCGTG 198
QY	121	GAGGCCGGGGCCGGGACCCCTGGGCCAACCCCTCGGCACCTCAAACCCGCTGAAGCTCCGTG 180
Dd	199	GAGGCCGGGGCCGGGACCCCTGGGCCAACCCCTCGGCACCTCAAACCCGCTGAAGCTCCGTG 258
QY	181	CTGACGACCTGGGCATCCCGCTGAACAACCTCATAGAAGGCTCCCAAGAAGTGTGTGGCT 240
Dd	259	CTGACGACCTGGGCATCCCGCTGAACAACCTCATAGAAGGCTCCCAAGAAGTGTGTGGCT 318
QY	241	GAGCTGGGTCCTCCAGGCCGTGGGGCCGTCGTAAGGCCCTCAAGGCCCTGCTGGGGGCCCTG 300
bB	319	GAGCTGGGTCCTCCAGGCCGTGGGGCCGTCGTAAGGCCCTCAAGGCCCTGCTGGGGGCCCTG 378

QY 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390

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; Sequence 407, Application US/09991073
; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Best Local Similarity 99.48; Pred. No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 79 ATGAGCTCGCGCCCTCTGGGGCTCTGGCGTGGCCCTGTCCTGACGCTCGGCTCGTGCT 138
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

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DB 259 CTGAGCAGCCTGGGGCATCCCCGTGAACCACTCATAGAGGGGTCCCAGAGTGTGTGGCT 318
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DB 319 GAGCTGGGTCCCAGCGCTGGGGGCGCTGAAGGCGCTGCTGGGGGCGCTG 378
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RESULT 14
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; Sequence 407, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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142 PRIOR FILING DATE: 1998-07-02
143 PRIOR APPLICATION NUMBER: 60/091978
144 PRIOR FILING DATE: 1998-07-07
145 PRIOR APPLICATION NUMBER: 60/091982
146 PRIOR FILING DATE: 1998-07-07

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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match          99.0%; Score 308.8; DB 9; Length 570;
Best Local Similarity 99.4%; Pred No. 4.6e-67;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 79 ATGAAGCTCGCGGCTCTCTGGGCTCTGCGGTGCGGCTCTGCTGAGCTCGGCTGCTGCT 138

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Db 259 CTGACAGCTCGGCGGCTCTGCGGCTCTGCGGCTCTGCGGCTCTGAGCTGCTGCTGCT 318

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Db 319 GAGCTGGGCTCGGCGGCTCTGCGGCTCTGCGGCTCTGAGCTGCTGCTGCTGCTGCTG 378

QY 301 ACAGTGTGTTGGC 312
Db 379 ACAGTGTGTTGGC 390

RESULT 15
JS-09-991-163-407
; Sequence 407, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
```



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QY 61 CGCAGAGGCGCCACAGAGGACCCCAAGTGTCCAGCGTTCGCGATCAGAGG 120
Db 61 CGCAGAGGCGCCACAGAGGACCCCAAGTGTCCAGCGTTCGCGATCAGAGG 120
QY 121 CAGGACACAGGAGCCAGAGAACTGGGCGCCCGCCCTGCTGCGGCGAGGAGCT 180
Db 121 CAGGACACAGGAGCCAGAGAACTGGGCGCCCGCCCTGCTGCGGCGG---AGGAAGCT 177
QY 181 CCTCACNAGAGGAAGTCTCCCTCACCCGCGCCAGCCCTCGAGGGGCGCGTGGGTC 240
Db 178 CCTCACNAGAGGAAGTCTCCCTCACCCGCGCCAGCCCTG-AGGAGGCGCGTGGGTC 236
QY 241 AGACCGCAAGAGGAGTGTGCGGCGCGGGTGGGCTTCGCGAGACAAGGCGCGGCTTCG 300
Db 237 AGACCGCAAGAGGAGTGTGCGGCGCGGGTGGGCTTCGCGAGACAAGGCGCGGCTTCG 296
QY 301 CTCTCTCAGAGGGCCCGCCAGCGCTTCAGAGGAAGTCTTCAGAGGCGCGGCGAGGAGG 360
Db 297 CTCTCTCAGAGGGCCCGCCAGCGCTTCAGAGGAAGTCTTCAGAGGCGCGGCGAGGAGG 356
QY 361 GGGCACGGGCTTCCAGGGCGCGCGCGCGAGGAGGAGTGGCCAGGGCACGGCGGTG 420
Db 357 GGGCACGGGCTTCCAGGGCGCGCGCGCGAGGAGGAGTGGCCAGGGCACGGCGGTG 416
QY 421 AGCGAGCGGCGAGGGCTTCTCAGAGAGCGCGGCGAGGCGCGGCTGGAGGGCGAGGA 480
Db 417 AGCGAGCGGCGAGGGCTTCTCAGAGAGCGCGGCGAGGCGCGGCTGGAGGGCGAGGA 476
QY 481 CCGGTATAGAAAGCCCTGCGCTTCGCGGCGAGCGGAGTTCGCCGCGCGCCCGA 540
Db 477 CCGGTATAGAAAGCCCTGCGCTTCGCGGCGAGCGGAGTTCGCCGCGCGCCCGA 536
QY 541 GCCCGCGCGCC 551
Db 537 GCCCGCGCGCC 547

RESULT 2
US-10-059-579-120
; Sequence 120, Application US/10059579
; Publication No. US20030138783A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: PACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (359)..(359)
; OTHER INFORMATION: n is any nucleotide
US-10-059-579-120

Query Match 60.1%; Score 338.4; DB 15; Length 1794;
Best Local Similarity 97.8%; Pred. No. 5.7e-70;
Matches 354; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 190 GAGGAGAGTCCCTCACCAGCCAGCTTCAGAGGGGCGCGTGGGTCAGACCCCAA 249
Db 812 GAGGAGAGTCCCTCACCAGCCAGCTTCAGAGGGGCGC--TGGGGTCAGACCCCAA 869
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QY 250 AGCAAGGTGCGGCGCGGGTGGGCTTCGCGAGACAAAGGCGGGGCTTCCTCTCTCAG 309
Db 870 AGCAAGGTGCGGCGCGGGTGGGCTTCGCGAGACAAAGGCGGGGCTTCCTCTCTCAG 929
QY 310 AGGCCCCAGCGCTTCCTCAAGAGAAAGTCTCAGAGCCCGGGCAGGAGAAAGGGGACGCGG 369
Db 930 AGGCCCCAGCGCTTCCTCAAGAGAAAGTCTCAGAGCCCGGGCAGGAGAAAGGGGACGCGG 989
QY 370 CTTCCAGAGGCGCGCGCGGCGAGGAGTGGCCAGGCGCGCTGAGGGAGCG 429
Db 990 CTTCCAGAGGCGCGCGCGGCGAGGAGTGGCCAGGCGCGCTGAGGGAGCG 1049
QY 430 GGCAGGCGCTTCTCAGAGGCGCGGGCGAGCGCGCTGGAGGGCGAGGACCGGGGTATA 489
Db 1050 GGCAGGCGCTTCTCAGAGGCGCGGGCGAGCGCGCTGGAGGGCGAGGACCGGGGTATA 1109
QY 490 AGAAGCTCTGCGGCTTCGCGGCGAGCGAGTTCGCGCGCGCGCGCGCGCGCG 549
Db 1110 AGAAGCTCTGCGGCTTCGCGGCGAGCGCGAGTTCGCGCGCGCGCGCGCGCGCG 1169
QY 550 CC 551
Db 1170 CC 1171

RESULT 3
US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196114
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196114

Query Match 25.5%; Score 143.6; DB 13; Length 533;
Best Local Similarity 94.8%; Pred. No. 1.4e-24;
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

QY 1 CGGCGCGGAGGCGCGCGGAGTGAGCGCTTCCTGCGCGCTTCACCTCCCGCAGG 60
Db 189 CGGCGCGGAGGCGCGCGGAGTGAGCGCTTCCTGCGCGCTTCACCTCCCGCAGG 130
QY 61 CGCAGAGGCGCCACAGAGACCCCGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 120
Db 129 CGCAGAGGCGCCACAGAGACCCCGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 70
QY 121 CA-GGAGACGAGGAGCCAGGAAGTGCAGCGCGCGCGCGCGCGCGCGCGCGAGG 179
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Db 69 CACGGACAGGAGCCAGGAACTGGCCGCCCC---CGCCCTGCTGGCGCGA-GGAAGC 14
QY 180 TCCCTCACCG 190
Db 13 TCCCTCACCG 3

RESULT 4

US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196114
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196114

Query Match 25.5%; Score 143.6; DB 16; Length 533;
Best Local Similarity 94.8%; Pred. No. 1.4e-24;
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;
QY 1 CGGCGGGAGCGCGGAGTGAAGGCTGATCGTCCCTGGCGCTCCACCTCCCGAGG 60
189 CGGCGGGAGCGCGGAGTGAAGGCTGATCGTCCCTGGCGCTCCACCTCCCGAGG 130
QY 61 CGCAGAAGCGCCACGAGGACCCCGAGTCCCGAGTTCGACGCTTGGGATCAGAGG 120
129 CGCAGAAGCGCCACGAGGACCCCGAGTTCGACGCTTGGGATCAGAGG 70
QY 121 CA-GGGACAGGAGCCAGGAACTGGCGGCCCGCCCTGCTGCGGAGGAGC 179
Db 69 CACGGACAGGAGCCAGGAACTGGCGGCCCC---CGCCCTGCTGGCGCGA-GGAAGC 14
QY 180 TCCCTCACCG 190
Db 13 TCCCTCACCG 3

RESULT 5

US-10-237-435-6
; Sequence 6, Application US/10237435
; Publication No. US20030124580A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Spiro, Peter A.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: LUNG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 US
; CURRENT APPLICATION NUMBER: US/10/237,435
; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 60/317,822
; PRIOR FILING DATE: 09-07-2001
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6

Query Match 20.6%; Score 116; DB 15; Length 561;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 GCTTTCTCAGGAGCGGGCGGAGGCGCGGCTGGAGGGGCGAGGACCGGGTATAAGAGC 495
Db 1 GCTTTCTCAGGAGCGGGCGGAGGCGCGGCTGGAGGGGCGAGGACCGGGTATAAGAGC 60
QY 496 CTCGTGGCCTTCCCGGCGCAGCGCAGGTTCCCGCGGCGCCCGAGCCCCCGCGCC 551
Db 61 CTCGTGGCCTTCCCGGCGCAGCGCAGGTTCCCGCGGCGCCCGAGCCCCCGCGCC 116

RESULT 6

US-10-426-002-18
; Sequence 18, Application US/10426002
; Publication No. US20040101876A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanging
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; APPLICANT: Rotem Sorek
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 26083
; CURRENT APPLICATION NUMBER: US/10/426,002
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-002-18

Query Match 15.5%; Score 87; DB 17; Length 527;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 465 GCTGAGGGCGGAGGACCGGGTATAAGAGCCTCGTGCTTGCCTGGGCGAGCCGCGAGT 524
Db 1 GCTGAGGGCGGAGGACCGGGTATAAGAGCCTCGTGCTTGCCTGGGCGAGCCGCGAGT 60
QY 525 TCCCGCGCGCCCGAGCCCGCGCC 551
Db 61 TCCCGCGCGCCCGAGCCCGCGCC 87

RESULT 7

US-10-211-958-27
; Sequence 27, Application US/10211859
; Publication No. US20030211096A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Marsters, Scot A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Pitti, Robert M.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stone, Donna M.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
 ; FILE REFERENCE: P2931R1C1
 ; CURRENT APPLICATION NUMBER: US/10/211,858
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: 60/014699
 ; PRIOR FILING DATE: 1996-04-01
 ; PRIOR APPLICATION NUMBER: 60/026943
 ; PRIOR FILING DATE: 1996-09-23
 ; PRIOR APPLICATION NUMBER: 60/059121
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: 60/062037
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: 60/063755
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: 60/066511
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066772
 ; PRIOR FILING DATE: 1997-11-24
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 258
 ; SEQ ID NO 27
 ; LENGTH: 569
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-211-858-27

Query Match 13.9%; Score 78; DB 13; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.5e-09;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCCTCGTGGCCTTCCCGGGCAGCCGCGAGGTTCCCGCGC 533
 Db 1 GCGAGGACCGGGTATAGAGCCTCGTGGCCTTCCCGGGCAGCCGCGAGGTTCCCGCGC 60

QY 534 GCCCGGAGCCCCCGCGC 551
 Db 61 GCCCGGAGCCCCCGCGC 78

RESULT 8
 US-10-210-951-27
 ; Sequence 27, Application US/10210951
 ; Publication No. US20030170228A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Marsters, Scot A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Pitti, Robert M.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria

; APPLICANT: Stone, Donna M.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
 ; FILE REFERENCE: P2931R1C1
 ; CURRENT APPLICATION NUMBER: US/10/210,951
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: 60/014699
 ; PRIOR FILING DATE: 1996-04-01
 ; PRIOR APPLICATION NUMBER: 60/026943
 ; PRIOR FILING DATE: 1996-09-23
 ; PRIOR APPLICATION NUMBER: 60/059121
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/062037
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: 60/063755
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063045
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/066511
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066772
 ; PRIOR FILING DATE: 1997-11-24
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 258
 ; SEQ ID NO 27
 ; LENGTH: 569
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-210-951-27

Query Match 13.9%; Score 78; DB 15; Length 569;
 Best Local Similarity 100.0%; Pred. No. 2.5e-09;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCCTCGTGGCCTTCCCGGGCAGCCGCGAGGTTCCCGCGC 533
 Db 1 GCGAGGACCGGGTATAGAGCCTCGTGGCCTTCCCGGGCAGCCGCGAGGTTCCCGCGC 60

QY 534 GCCCGGAGCCCCCGCGC 551
 Db 61 GCCCGGAGCCCCCGCGC 78

RESULT 9
 US-10-211-884-27
 ; Sequence 27, Application US/10211884
 ; Publication No. US20030175900A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Marsters, Scot A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Pitti, Robert M.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stone, Donna M.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
 ; FILE REFERENCE: P2931R1C1
 ; CURRENT APPLICATION NUMBER: US/10/211,884
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: 60/014699
 ; PRIOR FILING DATE: 1996-04-01
 ; PRIOR APPLICATION NUMBER: 60/026943

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; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 27
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-884-27

Query Match      13.9%; Score 78; DB 15; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      474 GCGAGCAGCGGTATAGAGCTCTGCGTCCGCGGACCGCAGGTTCCCGCGC 533
Db      1 GCGAGCAGCGGTATAGAGCTCTGCGTCCGCGGACCGCAGGTTCCCGCGC 60

QY      534 GCCCGAGCGCCCGCGCC 551
Db      61 GCCCGAGCGCCCGCGCC 78

RESULT 10
US-09-989-722-407
; Sequence 407, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084500
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
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; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
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; PRIOR APPLICATION NUMBER: 60/090862

; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;

Best Local Similarity 100.0%; Pred. No. 2.5e-09; Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAAGAGCCTCGTGGCCTTCCCGGGCAGCCGCGAGTTCGCCCGGC 533

Db 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCCTTCCCGGGCAGCCGCGAGTTCGCCCGGC 60

QY 534 GCCCGGAGCCCCCGCGCC 551

Db 61 GCCCGGAGCCCCCGCGCC 78

RESULT 11

US-09-989-723-407
; Sequence 407, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Nepier, Mary A.
; APPLICANT: Pal, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

1 PRIOR APPLICATION NUMBER: 60/091360
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3 PRIOR APPLICATION NUMBER: 60/091478
4 PRIOR FILING DATE: 1998-07-02
5 PRIOR APPLICATION NUMBER: 60/091544
6 PRIOR FILING DATE: 1998-07-01
7 PRIOR APPLICATION NUMBER: 60/091519
8 PRIOR FILING DATE: 1998-07-02
9 PRIOR APPLICATION NUMBER: 60/091626
10 PRIOR FILING DATE: 1998-07-02
11 PRIOR APPLICATION NUMBER: 60/091633
12 PRIOR FILING DATE: 1998-07-02
13 PRIOR APPLICATION NUMBER: 60/091978
14 PRIOR FILING DATE: 1998-07-07
15 PRIOR APPLICATION NUMBER: 60/091982
16 PRIOR FILING DATE: 1998-07-07
17 PRIOR APPLICATION NUMBER: 60/092182
18 PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGTATAGAACCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGC 533
Db 1 GCGAGGACCGGTATAGAACCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGC 60
QY 534 GCCCGAGCCCCCGCGCC 551
Db 61 GCCCGAGCCCCCGCGCC 78

RESULT 12

US-09-989-279-407

Sequence 407, Application US/09989279

Patent No. US20020072496A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C56

CURRENT APPLICATION NUMBER: US/09/989,279

CURRENT FILING DATE: 2001-11-19

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/043787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

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3 PRIOR FILING DATE: 1997-11-24
4 PRIOR APPLICATION NUMBER: 60/075945
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGAGCTCGTGGCTTGGCCGGGACGCCGAGGTTCCCGCGC 533
|||
Db 1 GCGAGGACCGGGTATAGAGAGCTCGTGGCTTGGCCGGGACGCCGAGGTTCCCGCGC 60

QY 534 GCGCGAGCGCCCGCGCC 551
|||
Db 61 GCGCGAGCGCCCGCGCC 78

RESULT 13

US-09-989-727-407
; Sequence 407, Application US/09989727
; Patent No. US20020072497A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2730PIC65

;; CURRENT APPLICATION NUMBER: US/09/989,727

;; CURRENT FILING DATE: 2001-11-19

;; PRIOR APPLICATION NUMBER: 60/049787

;; PRIOR FILING DATE: 1997-06-16

;; PRIOR APPLICATION NUMBER: 60/062250

;; PRIOR FILING DATE: 1997-10-17

;; PRIOR APPLICATION NUMBER: 60/065186

;; PRIOR FILING DATE: 1997-11-12

;; PRIOR APPLICATION NUMBER: 60/065311

;; PRIOR FILING DATE: 1997-11-13

;; PRIOR APPLICATION NUMBER: 60/066770

;; PRIOR FILING DATE: 1997-11-24

;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;

Matches 78; Conservative 0; Mismatches 0; Gaps 0;

474 GCGAGACCGGTATAGAGCTCTGTGCTTGCCTGCGGCGACCGCAGGTTCCCGCGCC 533

1 GCGAGACCGGTATAGAGCTCTGTGCTTGCCTGCGGCGACCGCAGGTTCCCGCGCC 60

534 GCCCGAGCCCCCGGCC 551

61 GCCCGAGCCCCCGGCC 78

RESULT 14

US-09-989-731-407

; Sequence 407, Application US/09989731

; Patent No. US20020103125A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC70
;; CURRENT APPLICATION NUMBER: US/09/989,731
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910

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;; PRIOR FILING DATE: 1998-04-28
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;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
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;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCAGGACCGGTATAGAGCCTGTCGCTTGGCCGGGACCGCAGGTTCCCGCGC 533
Db 1 GCAGGACCGGTATAGAGCCTGTCGCTTGGCCGGGACCGCAGGTTCCCGCGC 60
QY 534 GCCCGAGCCCCCGGCC 551
Db 61 GCCCGAGCCCCCGGCC 78

RESULT 15

US-09-989-732-407
; Sequence 407, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnucy, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

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?	PRIOR APPLICATION NUMBER:	60/091633
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match      13.9%; Score 78; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGGACCGGGTATAAGAAGCTCGTGGCCCTTGCCCGGCGAGCGCGAGGTTCCCGCGCC 533
Db 1 GCGAGGACCGGGTATAAGAAGCTCGTGGCCCTTGCCCGGCGAGCGCGAGGTTCCCGCGCC 60
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Qy 534 GCGCGGAGCCCCCGCGCC 551
Db 61 GCGCGGAGCCCCCGCGCC 78
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Job time : 417 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 16:42:04 ; Search time 86 Seconds
(without alignments)
3632.992 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence:

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	48.8	8.7	2561	4	US-09-616-289-48
C 4	48.4	8.7	4403765	3	US-09-103-840A-2
C 5	48.4	8.6	4411529	3	US-09-103-840A-1
C 6	48.2	8.6	4257	2	US-08-690-473-1
C 7	48.2	8.6	4257	3	US-09-259-821A-1
C 8	48.2	8.6	4257	3	US-08-843-659-1
C 9	48.2	8.6	12001	1	US-08-458-568A-11
C 10	47.4	8.4	6453	1	US-08-306-691B-14
C 11	47.4	8.4	6453	3	US-09-209-668-10
C 12	47.4	8.4	6453	3	US-09-356-952-8
C 13	47.2	8.4	3937	3	US-08-586-155-8
C 14	47.2	8.4	7218	1	US-08-232-463-14
C 15	47	8.3	1614	4	US-09-616-289-45
C 16	47	8.3	12425	2	US-09-616-289-50
C 17	46.8	8.3	4257	2	US-08-690-473-1
C 18	46.8	8.3	4257	3	US-09-259-821A-1
C 19	46.8	8.3	4257	3	US-08-843-659-1
C 20	46.8	8.3	12001	1	US-08-458-568A-11
C 21	46.6	8.3	932	1	US-08-458-912-1
C 22	46.6	8.3	932	1	US-08-461-179-1
C 23	46.6	8.3	932	1	US-08-459-254-1
C 24	46.6	8.3	932	1	US-08-459-255-1
C 25	45.8	8.1	35060	3	US-08-814-095-7
C 26	45.4	8.1	595	3	US-08-483-533-4
C 27	45.4	8.1	595	4	US-09-283-471A-4

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29	45.4	8.1	1327	4	US-09-283-471A-36	Sequence 36, Appl
30	45.4	8.1	1335	5	PCT-US91-06532-1	Sequence 1, Appl
C 31	45.4	8.1	15872	3	US-09-103-537-1	Sequence 1, Appl
C 32	45.4	8.1	15872	4	US-09-091-609-1	Sequence 1, Appl
C 33	45.4	8.1	15872	4	US-09-091-609-3	Sequence 3, Appl
C 34	45	8.0	765	4	US-09-252-991A-6511	Sequence 6511, Ap
C 35	45	8.0	864	4	US-09-252-991A-6520	Sequence 6520, Ap
C 36	44.2	7.9	364	4	US-09-621-976-17202	Sequence 17202, A
C 37	44.2	7.9	450	4	US-09-252-991A-6540	Sequence 6540, Ap
38	44	7.8	3695	1	US-08-091-569-1	Sequence 1, Appl
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40	44	7.8	3695	2	US-08-822-238-1	Sequence 1, Appl
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C 42	43.8	7.8	53526	3	US-08-658-136-2	Sequence 1, Appl
C 43	43.8	7.8	53577	3	US-08-658-136-1	Sequence 2, Appl
C 44	43.6	7.7	4638	4	US-09-023-655-4215	Sequence 1, Appl
C 45	43.4	7.7	2990	1	US-08-572-951-1	Sequence 1, Appl

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US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

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Best Local Similarity 48.7%; Pred. No. 0.035;
Matches 167; Conservative 0; Mismatches 173; Indels 3; Gaps 1;
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QY 281 GAGCAAGAGCCGGCGCTCTCTCTCAGAGGGGCCCGAGCGCTTCCAGAGAGGAGTCCT 340
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QY 341 CGAGGGCGGGCAGGAGAGGGGACCGGGTTCAGAGGGCGGGCGCGAGGAG 400
Db 22114 TGCGGGGGGGGGGGGGGGGGGGTTCGGGGTTCGGGGGGGGGGGGGGGGGG 22055
QY 401 TTGGCCAGGGCAGCGCGTTCAGCGGCGCGGCGAGGCTTTCTCAGGAGCGCGGCGAGGC 460
Db 22054 GTGG---GG 21998
QY 461 CGGCGCTGGAGGGGGGAGGACCGGGTATAAGACCTCTGTCGGCTTCCCGGGGCGAGCGCG 520
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ALIGNMENTS

QY 481 CCGGG 485
Db 606 CCGGG 602

RESULT 4

US-09-103-840A-2

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: PRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; FEATURE:

; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

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Best Local Similarity 46.7%; Pred. No. 0.1;
Matches 231; Conservative 0; Mismatches 253; Indels 11; Gaps 2;

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QY 61 CGCAGAAAGCGCCACAGAGAGACCCAGTCCCGAGTGTGCCAGCTCTGGGATCAGAG 120

Db 841169 CGGGCGCGGGGAAACGCCAGCATGCTGTTCGGCGCGCGGGGTCGGCGGTCGGCGG 841228

QY 121 CAGGACACGAGGAGCAGAGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Db 841229 ATTCTCGAACCGCGGTGCCACCGCGGGGCGAGCGGGGCGCGGGCGCGGGCGGT 841288

QY 181 CCTTACACNGAGGAGAGTCCCTCACCGGCGC---CAGCCCTGACGGGGCGCGTGG 237

Db 841289 TGGCGCGGAGGAGGAGCGGACGCGGCGGCTCGGGCAACCTCACTTGGCGGGCGCGCG 841348

QY 238 GTCCAGCCGAAAGCGAAGTGTGCGGCGCGGGTGGGCTTCGCGAGACAAAGCGCGGCG 297

Db 841349 GCGCGCGGCAACCGCGGACGCTCGCCACTGCTGATGCGGGCGCGGGACCGCGCG 841408

QY 298 TGCCTCTCTCAGAGGCGCCAGGCGCTGCGCAGAGAAATGCTTCGAGGCGCGGCGAGGA 357

Db 841409 CGCTAGTCGACGCGGGGATTCGGCGGGGCGAGCGGAGCGCGGCGCGCGCATGTT 841468

QY 358 AGGGGCGAGCGCTTCCAGGGCGCCCGCGCGCAGCAGAGTGGCCAGGGCA----- 412

Db 841469 CTTGCGCTCCGGCGGCTCCGGCGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 841528

QY 413 ---CGGCGGTGAGCGGAGCGGGCAGGGCTTCTCAGAGCGCGGGGAGCGCGGCGCTGG 469

Db 841529 CGCGCGGGGCGCGGGGCG 841588

QY 470 AGGGGCGAGGACCGG 484

Db 841589 CGGCGGAGCACCGG 841603

RESULT 5

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: PRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 8.6%; Score 48.4; DB 3; Length 4411529;
Best Local Similarity 47.9%; Pred. No. 0.13;
Matches 237; Conservative 0; Mismatches 247; Indels 11; Gaps 3;

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Db 838931 CGGACGCGGGGGCGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 838990

QY 61 CGCAGAAAGCGCCACAGAGAGACCCAGTCCCGAGTGTGCCAGCTCTGGGATCAGAG 120

Db 838991 CGGGGCGCGGAAACGCCAGCATGCTGTTCGGCGCGCGGGGTCGGCGGTCGGCGG 839050

QY 121 CAGGACACGAGGAGCAGAGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Db 839051 ATTCTCGAACCGCGGTGCCACCGCGGGGCGAGCGGGGCGCGGGCGGGCGGT 839110

QY 181 CCTTACACNGAGGAGTCCCTCACCGGCGC---CAGCCCTGACGGGGCGCGTGG 237

Db 839111 TGGCGCGGAAAGGAAACGCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 839170

QY 238 GTCCAGCCGAAAGCGAAGTGTGCGGCGCGGGTGGGCTTCGCGAGACAAAGCGCGGCG 297

Db 839171 GCGCGCGGCAACCGCGGACACTGCGCCACTGCTGATGCGGGGCGCGGGACCGCGG 839230

QY 298 TGCCTCTCTCAGAGGCGCCAGCGCTGCCAAGAGAAATGCTTCGAGGCGCGGGCAGGGA 357

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QY 358 AGGGGCGAGCGGCTTCCAGGGCGCCCGCGCGCAGCAGAGTGGCCAGGG--CACGCG 416

Db 839291 CTTGCGCTCCGGCGGCTCCGGCGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCG 839350

QY 417 CCGTACGCGAGCGGCGAGGGCTTTC-----TCAGAGCGCGGCGGCGCGGCGCTGG 469

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QY 470 AGGGGCGAGGACCGG 484

Db 839411 CGGCGGAGCACCGG 839425

RESULT 6

US-08-690-473-1/c

; Sequence 1, Application US/08690473

; Patent No. 5876923

; GENERAL INFORMATION:

; APPLICANT: Leopardi, Rosario

; APPLICANT: Roizman, Bernard

; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN

; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS

RESULT 10

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US-08-306-691B-14/c
/ Sequence 14, Application US/08306691B
/ Patent No. 5734039
/ GENERAL INFORMATION:
/ APPLICANT: Calabretta, Bruno
/ APPLICANT: Skorski, Tomasz
/ TITLE OF INVENTION: ANTISENSE
/ TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
/ NUMBER OF SEQUENCES: 55
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seidel, Gonda, Lavoragna & Monaco, P.C.
/ STREET: Two Penn Center, Suite 1800
/ City: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19102
/ COMPUTER READABLE FORM.

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1  COMPUTER READABLE FORM:
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3  MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
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5  COMPUTER: IBM PS/2
6
7  OPERATING SYSTEM: MS-DOS
8
9  SOFTWARE: WordPerfect 5.1
10
11 CURRENT APPLICATION DATA:
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13 APPLICATION NUMBER: US/08/306,691B
14
15 FILING DATE: September 15, 1994
16
17 CLASSIFICATION: 514
18
19 PRIOR APPLICATION DATA:
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21 APPLICATION NUMBER:
22
23 FILING DATE:
24
25 ATTORNEY/AGENT INFORMATION:
26
27 NAME: Monaco, Daniel A.
28
29 REGISTRATION NUMBER: 30,480
30
31 REFERENCE/DOCKET NUMBER: 8321-8
32
33 TELECOMMUNICATION INFORMATION:
34
35 TELEPHONE: (215) 568-8383
36
37 TELEFAX: (215) 568-5549
38
39 TELEX: No. 5734039e
40
41 INFORMATION FOR SEQ ID NO: 14:
42
43 SEQUENCE CHARACTERISTICS:
44
45 LENGTH: 6453 base pairs
46
47 TYPE: nucleic acid
48
49 STRANDEDNESS: single
50
51 TOPOLOGY: linear
52
53 US-08-306-691B-14

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Query Match 8.4%; Score 47.4; DB 1; Length 6453;
Best Local Similarity 46.5%; Pred No. 0.15;
Matches 255; Conservative 0; Mismatches 287; Indels 6; Gaps 3;

9	QY	GAGCGGCGGGAGTGAGGCTGTATCGTCTCGCGCCTCCACCTCCCGACGCGCAGAG	68
883	Db	 GACGCCCGGGTGTGAGGCGCGGCGCGAGGCTCCCGGTACGCGGGCTGGGGACC	824
69	QY	GCGCCACGAGGACCCCACTGTCGCCAGCTTGCCA CGGTCTGGGATCAGAGCAGGGACC	128
823	Db	 GTGCCACGCGAGGCCACCGGTGGGGCCCGGATTC CGCAGGCCCCACAGGAGGAGGGG	764
129	QY	AGGAGCCAGGAACTGCGCGCGCCCGCGCCCTCGCCCTGGCGCGAGGAAGTCCCTCACC	188
763	Db	 CCCCCGCGCGCAGCCCCGAGCGCCGTCTACCTGTGCCCGCGGCGCCGCCCC - GGCC	705
189	QY	NGAGGAGAGTTCCTCCCTCACCCGCGCCAGCCCTCAGCGGGCGCGGTGGGGTCAGACCGCA	248
704	Db	 CACCCACCGCGCGCGCGCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	645
249	QY	AAGCGAAGTCCGGGCGGGGTGGCGCTCGCGGAGCAAAAGGCCGGCGCTGCTCTCTCA	308
644	Db	 CCGCGGTATTGTGCGCGCTGGGGGCGAGAGGGCGCGCGGCCCGGCGATCCCTGCGCC	585
309	QY	GAGGCCCCACGCGCTCCCAAGAGGAGTCTCTGAGGCCCGCGCAGGAGAGGGGGCAGG	368
584	Db	 GCATCAACGTTACAGGC - GGGACTGCCCGGGGCCAGGGCCCGGGCGCGAGCGCGGG	527

369	QY	GTTTCCCAAGGCGCCGCGCGCGAGCAAGTTGGCCAGGGCACGCGCCGCTGAGCGGAGC	428
526	Db	CGCGGGCGGGGCGGGGCGCGCGGTTTCGCCCGCGCATGGGC--TCCGTCCGCGCGCG	470
429	QY	GGGCAAGGCTTTCACAGAGCGCGGGCGAGCGCGCGCTCGAGGGGCGGAGACCGGGTAT	488
469	Db	GTGCGGCTCGGGTTGCGGGCGCACAGGACCGGGGCGGAGACTCGGCGCGGGCCCTGCGCAC	410
489	QY	AAGAAGACCTCGTGCGCTTTCGCCGGGCGACCGCGAGTTCCCGCGCGCCCGAGCCCCCGC	548
409	Db	GCCCGCGCCCGCGCGCTTCGCTGTGCCAGGCGGGCGCTACCATTTGCTGCGCGCATCG	350
549	QY	GCCCGGCC	556
349	Db	GCCCGGCC	342

RESULT 11
 US-09-209-668-10/c
 ; Sequence 10, Application US/09209668A
 ; Patent No. 6114517
 ; GENERAL INFORMATION:
 ; APPLICANT: Monha, Brett P.
 ; APPLICANT: Xu, Xiaoxing S.
 ; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
 ; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
 ; FILE REFERENCE: ISPH-0336
 ; CURRENT APPLICATION NUMBER: US/09/209,668A
 ; CURRENT FILING DATE: 1998-12-10
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 6453

RESULT 11

```

RESULT 11
US-09-209-668-10/c
/ Sequence 10, Application US/09209668A
/ Patent No. 6114517
/ GENERAL INFORMATION:
/ APPLICANT: Monia, Brett P.
/ APPLICANT: Xu, Xiaoxing S.
/ TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
/ FILE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
/ FILE REFERENCE: ISPH-0336
/ CURRENT APPLICATION NUMBER: US/09/209,668A
/ CURRENT FILING DATE: 1998-12-10
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 6453
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1664)..(1774)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (2042)..(2220)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (2374)..(2533)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3231)..(3350)
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: V00574/Genbank
/ DATABASE ENTRY DATE: 1991-01-03
US-09-209-668-10

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Query Match 8.4%; Score 47.4; DB 3; Length 6453;
Best Local Similarity 46.5%; Pred. No. 0.15;
Matches 255; Conservative 0; Mismatches 287; Indels 6; Gaps 3;

9	GAGGGGCGGGAGTGAGGCGCTGATCGTCCCTGGGGCTTCCACCTCCACAGCGCAGAG	68
QY		
883	GACCCCCCGGGTGTAGGGCGCGGGCCGAGAGCTCCCGGTACGCGCGCTGGGGACC	824
Db		
69	GCGGCCACGAGGAGCCCCCAGATGTCGCCAGCTTGCCAGGTCTGGGATCAGAGCAGGGACC	128
QY		
823	GTGCCACAGCGAGGCCACGGGTGGGGCCCCGATTCCCGACGCCCCCAGGAGAGAGGGG	764
Db		
129	AGGAGTCAGGAACTGCGCGCGCCCCCGCCCTGCCCTGGCGCGAGGAGTCCCTCTACC	188
QY		
763	CCCCG-CCGCGCAGCCCCCGAGCCCGCTCACTGTGCGCGGGCCCCGCC-GGCC	705
Db		
189	NGAGGGAAGTCCCTTCAACCCGCCCCAGGCCCTGCGAGGGGGCGGTGGGGTCAGACCGCA	248
QY		
704	CCACCAACCGCGCGCGCGCGCTTACGCGCCCGCGCCCGCGCCCCCGCGCCCGG	645
Db		

QY 249 AAGCGAAGTTCGGGCGGGTGGCCCTCGCGGAGACAAAGGCGCGGCTGCCTCTCTCA 308
 Db 644 CCGCGCGTATTGTCGCGCCTGGGGGCGAGAGGCGCGCGCGCCGATCCTGCCCC 585
 QY 309 GAGGGCCCCAGCGCTGCAAGAGGAAGTCTCGAGCCCGGGCAGGAAGGGGACGG 368
 Db 584 GCATCACCGTTACAGGC--GCGACTGCCCCGGGGCAGGGCCGGGGCGAGGCCGG 527
 QY 369 GTTCCAGAGGCGCGCGCGCGCAGCAGGGAAGTTGGCAGGGCACGCGCCGTGAGCGGAGC 428
 Db 526 GCGGGGCGGGGCGGGCGCGGTTGCGCCCGCGCATGGGC---TCCGTCCGCGCGG 470
 QY 429 GGGCAGGCTTCTCAGAGCGCGGGCGAGGCTTCCCGCGCGCGCGCGCGCGCGGATAT 488
 Db 469 GTGCGGCTCGGTTGCGGGGCGAGGGCACGCGGCGCGGAGACTCGGGCGGGCTGCGCAC 410
 QY 489 AAGAAGCTCTGTCGCTTCCCGGGCAGCGAGTTCCCGCGCGCGCGCGCGCGCGCGC 548
 Db 409 GCCCGCGCGCGCGCTGCTGTCAGGGCGGCGCTACCATTTGGCTGCGCGCATCGG 350
 QY 549 GCCCGGCC 556
 Db 349 GCCCGGCC 342

RESULT 12

US-09-356-952-8/c
 ; Sequence 8, Application US/09356952
 ; Patent No. 6117663
 ; GENERAL INFORMATION:
 ; APPLICANT: Boriack-Sjodin, Ann
 ; APPLICANT: Margalit, S. M.
 ; APPLICANT: Bor-Sogai, Dafna
 ; APPLICANT: Cole, Philip
 ; APPLICANT: Kuriyan, John
 ; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
 ; FILE REFERENCE: 600-1-228N
 ; CURRENT APPLICATION NUMBER: US/09/356,952
 ; CURRENT FILING DATE: 1999-07-19
 ; EARLIER APPLICATION NUMBER: 60/093,631
 ; EARLIER FILING DATE: 1998-07-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 6453
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-356-952-8

Query Match 8.4%; Score 47.4; DB 3; Length 6453;
 Best Local Similarity 46.5%; Pred. No. 0.15;
 Matches 255; Conservative 0; Mismatches 287; Indels 6; Gaps 3;
 QY 9 GAGGGCGCGGAGTTCAGCGCTCATGTCCTGGCGGCTCCACCTCCAGGCGCAGAAG 68
 Db 893 GAGCGCCCGGGTGTAGGGCGCGCGGCGCGAGGCTCCCGGGTACCGCGCGTGGGGACC 824
 QY 69 GCGCCCGCAGGAGACCCAGTGCAGCGTTCGACAGGCTCGGATCAGAGCAGGAGC 128
 Db 823 GTGCCAGCGCAGGCGCAGGGTGGGGCGCGGATTCGCGAGCCCGCAGGAGGAGGGG 764
 QY 129 AGGGAGCCAGGAATTCGCGCGCGCGCGCGCTGCTGCGCGAGGGAAGCTCCCTCACC 188
 Db 763 CCGCCCGCGCGCAGACGCCCGCAGCGCGCTACCTGTGCGCGCGCGCGCGCGCGCG 705
 QY 189 NGAGGGAAGTCCCTTACCCCGCGCGCGCGCTGCGAGGGGGCGCGTGGGGTACAGCGCA 248
 Db 704 CCACCCAGCCCGCGCGCGCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 645
 QY 249 AAGCGAAGTTCGGGCGGGTGGGCTTCGCGGAGACAAAGGCGCGGCTGCTCTCTCA 308
 Db 644 CCGCGCGTATTGTCGCGCCTCGGGGCGAGAGGGCGCGCGCGCGCGCGGATCCCTGCC 585

QY 309 GAGGGCCCCAGCGCTCCCAAGAGGAAGTCTCTGAGCCCGCGCAGGAAGGGGACCGG 368
 Db 584 GCATCACCGTTACAGGC--GCGACTGCCCCGGGGCAGGGCCGGGGCGAGGCCGG 527
 QY 369 GTTCCAGAGGCGCGCGCGCGCAGCAGGGAAGTTGGCAGGGCACGCGCCGTGAGCGGAGC 428
 Db 526 GCGGGGCGGGGCGGGCGCGGTTGCGCCCGCGCATGGGC---TCCGTCCGCGCGG 470
 QY 429 GGCAGGCTTCTCAGAGCGCGGGCGAGGCTTCCCGCGCGCGCGCGCGCGGATAT 488
 Db 469 GTGCGGCTCGGTTGCGGGGCGAGGGCACGCGGCGCGGAGACTCGGGCGGGCTGCGCAC 410
 QY 489 AAGAAGCTCTGTCGCTTCCCGGGCAGCGAGTTCCCGCGCGCGCGCGCGCGCGCGC 548
 Db 409 GCCCGCGCGCGCGCTGCTGTCAGGGCGGCGCTACCATTTGGCTGCGCGCATCGG 350
 QY 549 GCCCGGCC 556
 Db 349 GCCCGGCC 342

RESULT 13

US-08-586-165-8/c
 ; Sequence 8, Application US/08586165
 ; Patent No. 6054298
 ; GENERAL INFORMATION:
 ; APPLICANT: Laufer, Edward M.
 ; APPLICANT: Orozco, Olivia B.
 ; APPLICANT: Tabin, Clifford J.
 ; TITLE OF INVENTION: Fringe Proteins and Pattern Formation
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/586,165
 ; FILING DATE: 16-JAN-1996
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: HU95-05
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3937 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-586-165-8

Query Match 8.4%; Score 47.2; DB 3; Length 3937;
 Best Local Similarity 47.7%; Pred. No. 0.16;
 Matches 169; Conservative 0; Mismatches 183; Indels 2; Gaps 1;
 QY 207 CCGCGCCCGAGCCCTGTCAGGGGGCGCGTGGGGTCAGACCCGAAAGCGAGGTGGGGCGG 266
 Db 455 CCCATCGGAGCCCTCCGCGAAGGGCACGGGTACCGGGGAGCCCGGCCGCCGCCCGCG 396
 QY 267 GGGTGGGCTCGCGGAGACAAAGGCGCGGCGCTGCTCTCTCAGAGGGGCCCGAGCGCTGCG 326

Db 395 GTCCCGACCGCCGCGCGTCCCGGACGTCGCTCCCGCGGCGCGCCCTCCCGC 336
QY 327 CAAGAGGAAGTCTCGAGCCCGGGCAG--GGAAGGGGCGACGGGCTTCCAGGGCGCGC 384
Db 335 TTCCGGGAGGGCTGCTGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276
QY 385 CGCGCGCAGCAGGAAGTTGGCCAGGCGACGCGCGGTGAGCGGAGCGGCGAGGCTTTCTCA 444
Db 275 TGTCCCGCGGGCGAGCAGCAGCAGGAGACGCGCGCGCGGTGACCGACAGCAGGAAGCA 216
QY 445 GGAGCGCGCGCGCGCGCGCTGGAGGGCGCGAGACGGGTATAAGAGCTTCTGCGCC 504
Db 215 GCTCTGCGGAGCCCGCAGCAGAGCTGCTCATGTGCGGCGCCCGCCCGCGCGCG 156
QY 505 TTGCGCGGCGCGCGCGCGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
Db 155 CTGCGCGCGCGCGCTCATGCGCCCGCGGAGCGCGCGGAGCGGTTTCCCGCGCG 102

RESULT 14

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F15

US-08-232-463-14

Query Match 8.4%; Score 47.2; DB 1; Length 7218;
Best Local Similarity 4.4%; Pred. No. 0.17;
Matches 13; Conservative 171; Mismatches 114; Indels 0; Gaps 0;

QY 223 AGGGGGCGCGTGGGTGAGTCCAGACGCAAGAGTGGCGCGCGGTGGCGCTCCGCGA 282
Db 1339 RRR 1280
QY 283 GACAAAGCCCGGCTGCTCTCTCAGAGGCGCCAGGCGCTGCCAAGAGGAAGTCTCG 342
Db 1279 RRR 1220
QY 343 AGGCCCGGCGAGGAAGGGGCGACGGGCTTCCAGGCGCCCGCGCGCAGCAAGTT 402
Db 1219 RRR 1160
QY 403 GCGCAGGCGACGCGCGTGCAGCGGCGGCGAGGCGCTTCTCAGAGCGCGCGCGCAGCGC 462
Db 1159 RRR 1100
QY 463 CGCTGAGGGCGGAGGACCGGCTATAGAGCCTCTGCGCTTGGCGCGCGCGCAGCGC 520
Db 1099 RRR 1042

RESULT 15
US-09-616-289-45
; Sequence 45, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-616-289-45

Query Match 8.3%; Score 47; DB 4; Length 1614;
Best Local Similarity 46.6%; Pred. No. 0.17;
Matches 257; Conservative 0; Mismatches 286; Indels 9; Gaps 3;
QY 1 CGGCGCGGAGGGCGCGCGGAGTGAGGCTGTATGTCCTTGGCGCGCTTCCACTCCCGAGG 60
Db 306 CGGCGCGGAGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365
QY 61 CGCAGAGGCGCCCGCAGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 366 CG 425
QY 121 CAGGGACCGAGGAGCCAGGAATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 426 CG 485
QY 181 CCTTCAACGAGGAGAGCTCCCTCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 233

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Db 486 TGGCCCCCGCGCAGCGGGCCCCCGCGGCGACGCGGGCCGCGCCCCCTGGCCCGCGCGCGCC 545
QY 234 TGGGGTCAGACCGCAAGCGAAGTGGCGGCCCGGGGTGGGCTTCGGGGAGACAAAGGCCG 293
Db 546 CGGCGCAGCGCGCTCCCCCGCGGTGGCGCCCCCGCGCGCGCGCGCCCCCGCGCC 605
QY 294 GGCCTGCCTCTCTCAGAGGSCCCCGAGCGCTGCGAAGAGGAAGTCTCTGAGGCCCCGGGCA 353
Db 606 CGCCGTGCGCGCCCGGAGCGCGCGCTGCGCGCGCGCGCCACAGCCCGCGCGCGCGCCACA 665
QY 354 GGGAGGGGGCACGCGGCTTCCAGGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 413
Db 666 GCAGCAGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 725
QY 414 GGCCTGTAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 473
Db 726 CGGCG-GCGCGCGCGCGCGCGCGTGAAGCTGCGGGAAGTCTGTGCGTACCTCGGGGGCAGCG 784
QY 474 GCGAGGACCG-GGTATAAGAGCCTGTGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCG 532
Db 785 GCGGCGCGCGCGCGCGTCAACCGCGCGCGCGCGTGCAGGGGCTGCTGGAAGGAGGGCG 844
QY 533 CGCCCCGAGGCC 544
Db 845 CGGCTCGAGGCC 856
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Search completed: June 6, 2004, 18:43:53
Job time : 99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 16:39:00 ; Search time 2620 Seconds
(without alignments)
6416.949 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence: 1 cggccggggaggcggccggg.....cccgcccgccggcggggagg 563

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rpd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.4	15.7	982	13	BX415111 BX415111
2	82.2	14.6	982	13	BX415111 BX415111
3	81.6	14.5	1203	29	CNS015Y4
4	81.2	14.4	935	29	CNS006XK

5	80.2	14.2	1313	29	AG032885
6	80	14.2	1281	12	BG852363
7	77.4	13.7	1284	12	BM547577
8	77.2	13.7	925	29	CNS0091P
9	75.8	13.5	1101	29	CNS017SY
10	74.8	13.3	932	29	CNS0072Q
11	74.6	13.3	1628	29	CG57066
12	74.4	13.2	1065	13	BQ681076
13	74.2	13.2	888	12	BG809572
14	74	13.1	1040	12	BG809572
15	73.6	13.1	949	29	AG043499
16	73.6	13.1	1132	14	CK210297
17	73.4	13.0	1035	29	CNS017KO
18	73.4	13.0	1201	9	AL539262
19	73	13.0	776	29	CNS010RY
20	73	13.0	1100	29	CNS016KD
21	73	13.0	1143	13	BU502934
22	72.6	12.9	1201	13	HX405071
23	72.4	12.9	737	14	CF217719
24	72.4	12.9	873	12	BG844318
25	72.4	12.9	1085	29	AG152796
26	72.2	12.8	937	29	AG080291
27	72.2	12.8	1030	29	AG126333
28	72.2	12.8	1273	12	BM562099
29	72	12.8	924	13	BX442207
30	71.8	12.8	660	28	BZ690979
31	71.6	12.7	1073	13	BQ721449
32	71.6	12.7	1144	13	EX415926
33	71.2	12.6	822	28	AZ187356
34	71.2	12.6	970	29	CNS010C9
35	71	12.6	1100	29	AG161988
36	71	12.6	1201	13	EX405071
37	71	12.6	1299	12	BM909809
38	71	12.6	1581	29	AG052690
39	70.6	12.5	847	29	AG076581
40	70.4	12.5	925	29	CNS0091P
41	70.4	12.5	1101	29	CNS00397
42	70.2	12.5	822	29	AG154144
43	70.2	12.5	932	29	CNS0072Q
44	70	12.4	903	28	BZ051933
45	70	12.4	1021	13	BQ434910

ALIGNMENTS

RESULT 1
BX415111/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

982 bp mRNA linear EST 15-MAY-2003
BX415111 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004YI20
5-PRIME, mRNA sequence.

1 GI:30765470

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 982)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0CAP004BE10QF1.

Location/Qualifiers

1..982

/organism="Homo sapiens"

FEATURES
source

ACCESSION	AL066051
VERSION	AL066051.1
KEYWORDS	GI:4945019
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Ephyroides; Drosophilidae; Drosophila.
REFERENCE	1. (bases 1 to 935)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999)
	Genoscope - Centre National de Sequencage :

RESULT 5	LOCUS	DEFINITION	ORGANISM
AG032885	LOCUS	1313 bp DNA linear	GSS 01-NOV-2001
AG032885	DEFINITION	Pan troglodytes DNA, clone: PEB-007M05.F, genomic survey sequence.	
AG032885	ACCESSION		
AG032885	VERSION		
AG032885.1	KEYWORDS	GI:16559758	
AG032885.1	SOURCE	GSS.	
AG032885.1	ORGANISM	Pan troglodytes (chimpanzee)	
AG032885.1	REFERENCE	Pan troglodytes	
AG032885.1	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
AG032885.1	REFERENCE	1	
AG032885.1	AUTHORS	Fujiyama A., Hattori, M., Toyoda A., Tavor, T.D., Yada, T.,	

Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 1313)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbessgsc.riken.go.jp, URL:http://hnp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-007M05.F"
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
Query Match 14.2%; Score 80.2; DB 29; Length 1313;
Best Local Similarity 43.5%; Pred. No. 0.00051;
Matches 232; Conservative 0; Mismatches 301; Indels 0; Gaps 0;
QY 27 GCCTGATGTCCTCGCGCTCCACCTCCAGGCGCAGAGCGCCACGAGGACCCCG 86
Db |||||
QY 412 GCCCGCCG 471
Db |||||
QY 87 AGTGCCCGACGTTGGCCAGGTTGGGATCAGAGGACAGGACAGGAGGAGGACTGG 146
Db |||||
QY 472 CG 531
QY 147 CG 206
Db |||||
QY 532 GCG 591
QY 207 CG 266
Db |||||
QY 592 GCG 651
QY 267 GGTGCGCGCTCGCGGAGACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 326
Db |||||
QY 652 CG 711
QY 327 CAAGAGGAGTCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 386
Db |||||
QY 712 CG 771
QY 387 GCGCGAGCAGGAGTTGGCCAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
Db |||||
QY 772 CGGCG 831
QY 447 AGCG 506
Db |||||
QY 832 CG 891
QY 507 GCG 559
Db |||||
QY 892 GNGCGGCG 944

RESULT 6
BG852363/c
LOCUS 1281 bp mRNA linear EST 29-MAY-2001
DEFINITION 1024034A03.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BG852363
VERSION 1
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
1 (bases 1 to 1281)
Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1..1281
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 14.2%; Score 80; DB 12; Length 1281;
Best Local Similarity 46.9%; Pred. No. 0.00055;
Matches 265; Conservative 0; Mismatches 297; Indels 3; Gaps 2;
QY 1 CG 60
Db 1068 CG 1009
QY 61 CGCAGAGCG 120
Db 1008 CG 949
QY 121 CAGGAGAC CAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 948 GGGNGCG 889
QY 191 CCTCTACCGAGGAGAGTCTCCCTTACCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 888 CCG 829
QY 241 AGACCGGAAAGCGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 828 GCG 769

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QY 301 CTCCTCTCAG--AGGGCCCAAGCGGCTTCCCAAGAGAAAGTCTCTGAGGCCCGGGCAGGGAA 358
Db 768 CGGGGNGCGCCCGGNGNCCCGGGGGCGCGCGGGCCNGCGCGGGGCGCGGGGGGGCG 709
QY 359 GGGGGCAGGGCTTCCAGAGGCCCGCGCGCGCAGCAGGAAGTTGGCCAGGGCACGGCCG 418
Db 708 GCGGGCGGGCGNGGGGGGGGGCGCGCGCGCGCGCGCCCGCGGNGNCCCGGGGGGGCG 649
QY 419 TGAGCGGAGGGGGCAGGCGCTTCTCAGAGCGCGGGCGAGCGCGGCGCTCGAGGGGGCGAG 478
Db 648 CGCCCGCGGGGGGNGCCGCGCGNCGCGCGCGCGCGCGCGCGCGGGGNGGGGGGCC 589
QY 479 GACCGGTATAAGAGCCTCTGTGCGCTTCCCGCGCGCAGCGCAGGTTCCCGCGCGCCCC 538
Db 588 GGGCGGGCGCGCGCGCC-GGGGCGGGCGCGCGGGCGGGGGCGGGCGGGGGGGCG 530
QY 539 GAGCCCCCGCGCGCGCGGGGAGG 563
Db 529 CGGGCGGGCGCGCGCGCGCGCG 505

RESULT 7
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LOCUS BM547577 1284 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6507057 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727629
5', mRNA sequence.
ACCESSION BM547577
VERSION BM547577.1 GI:18781461
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1284)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12722 row: a column: 06
High quality sequence stop: 249.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5727629"
/tissue_type="hippocampus"
/lab_host="PH108"
/clone_lib="NIH MGC 124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dr primed and directionally
cloned (Scorv site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN
Query Match 13.7%; Score 77.4; DB 12; Length 1284;
Best Local Similarity 45.6%; Pred. No. 0.0015;
Matches 259; Conservative 0; Mismatches 303; Indels 6; Gaps 1;
QY 1 CGGCCGGAGGGCGGGAGTGAGCGCTGATCGCTTCCTGGCGCTCCACTCCCGAGG 60
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Db 1219 CGNCCGCGNGNCCNNNGCGGGCGCGCNCNCCCGGGCGGGCGCGCGNCGCCCGCGCCCGC 1160
QY 61 CGCAGAAGCGCGCCCAAGAGACCCCGAGTGCCCGCAGAGTTGCGCACGGTCTCGGATCAGAG 120
Db 1159 CGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1100
QY 121 CAGGGACCAAG-----GGAGCCAGGAACATGCGCGCGCCCGCGCGCGCGCGCGCGCGCG 174
Db 1099 CGGGCGCGNCGGGGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1040
QY 175 GAAGTCTCTCAACNAGAGGAAGTCTCCCTCAACCCCGCGCGCGCGCGCGCGCGCGCGCG 234
Db 1039 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 980
QY 235 GGGGTGAGACCGCAAGAGCGAAGTGGGGGGCGGGGTGGGGCTTCGGGAGACAAAGGCCGG 294
Db 979 GCGNNNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 920
QY 295 GCCTGCTCTCTCAGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 354
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QY 355 GGAAGGGGGCAGCGGCTTCCCAAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414
Db 859 GGGGGCGCGNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 800
QY 415 GCGGTGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 474
Db 799 CGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
QY 475 CGAGGACCGCGGTATAAGAAAGCCTCGTGGCGCTTGGCCCGGGCAGCGCGCGCGCGCG 534
Db 739 CGGCNCCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 580
QY 535 CCCCAGAGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 680
Db 679 CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652

RESULT 8
CNS0091P/c
LOCUS CNS0091P 925 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACH19D16 of RPCL-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL053013
VERSION AL053013.1 GI:4934461
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCL-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be

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found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

```

1. 925
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
/note="and : TET13"
source

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ORIGIN

Query Match	13.7%	Score	77.2;	DB	29;	Length	925;
Best Local Similarity	13.3%;	Pred. No.	0.0015;				
Matches	48;	Conservative	185;	Mismatches	128;	Indels	0;
Gaps	0;						
QY	178	GTCTCCCTCACCNAGAGGAAGCTCCCTCACCCGGCCAGCCCTCGACGGGGCGCGTGGG	237				
DB	918	SCSCSBBSCSSSMWTSNNSBSCSCSBBSSSSTSSMSSSSBSSSSSGSSSSSGTSSA	859				
QY	238	GTTCAGACCGCAAGCGAAGTGGCGGGCGGGGTGGGCTTCGCGAGACAAGGCGCGGCC	297				
DB	858	CVKCNASSCCGCGMABCMBCSSSSSCGSARGVKVRASGAGKRGGGSGGASASH	799				
QY	298	TGCGCTCTTCAGAGGGCCCCAGCGCTTCCAAAGAGGAAGTCTCTCGAGGCCGCGCAGGA	357				
DB	798	SSSSACBSSSSSCASCSWSSSSSSSSRSRGGGAGSGGSSSSSSSSSSASAGSV	739				
QY	358	AGGGGCGACGGGTTTCCAGGGCGCGCGCGCAGCAGGAAGTTGCCAGGGCACGGCC	417				
DB	738	SSASSSSSCSSSVSSSVASSMSCSBBSSSSASASSSSSSASCSCCCTTSSWSC	679				
QY	418	GTACGCGAGCGGCGAGGGCTTCTCAGAGCGCGCGCGAGCGCGCTGTGAGGGCGGA	477				
DB	678	STGASMAARSSSSSSSSCSSSMASSASSSASSSSSSSSSSSGSACGBSMSSGGG	619				
QY	478	GGACCGGGTATAGAAGCCTCTGTGGCTTGCCTGGCGGCGACGCGAGGTTCCCGCGCGCC	537				
DB	618	SGSVASSSGMSSSVSSSGRRSSSGGGGGVGGGSSSSSGSGSGSGSVCSGCGMCRC	559				
QY	538	C	538				
DB	558	S	558				

RESULT 9	CNS017SY	1101 bp	DNA	linear	GSS 26-JUL-1999
LOCUS	CNS017SY				
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL108460				
VERSION	AL108460.1	GI:5628764			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 1101)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBel0BAC11.				

FEATURES

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source
1. ll01
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="RAC3710BAC"
/parent="ll01"
/placement="PBE10BAC11"
/feature="356"
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QY	126	ACACGGGAGCCAGGAAC	TGCGCGCGCCCGCCCTCCCTGCGCGGAGGAAGCTCCCTC	185	
Db	635	ACACGSGAGCGRRKGC	AAKCSAGMSCCGRSGSGSSCCGGKAKGVGRGRVCCAGGG	694	
QY	186	ACCKAGAGGAAGCTTCC	CCCTCACCCGGGCCACGCCCTCAGCGGGGGCGCTGGGGTCAGAC	245	
Db	695	ASCAKMAADCGCCCAKMAC	SSSSASSSSSSCASTSSSASRGVMVSSCACSGSGSGGASA	754	
QY	246	GCAAGAGCAAGTCCGGG	CGGGTGGCTCGCGAGACAAAGGCCGGGCTGCTCTC	305	
Db	755	CGSAGGSGRGGSGCC	ASSGVCAACSSASCSSASMCVSSSSSSCSASCSCCGVSS	814	
QY	306	TAAGAGGCCCCACGCGCT	--GCCAAGAGGAAGTCTTCAGGCGCGGGCAGGAAGGGG	363	
Db	815	CSAVSASASAVMSKVASA	VASCSAVASGMSAGAVSSSCRSSVASVSAASVSSSVSSS	874	
QY	364	CACGGCTTCCAGGGCC	CGCCGCGCAGCAAGTGTGGCCAGGCGACGCGCTGAGC	423	
Db	875	SSSSVVSAAVAS	SSSSASASAAVAASVSVSVASVVSSSSSSCSSSSASVVVSA	934	
QY	424	GGACGGCGCAGGGCTTCT	CAGGACCGGGCGAGCGCGCTGAGAGGGCGAGCACCG	483	
Db	935	SVAASASVSSSSSVST	SSSASVSVSVASVMSAVVSSSASSSSVSVSVVAASAA	994	
QY	484	GGTATAGAAGCCTCTG	GCCCTTCCCGGGCAGCCCGCAGTTCCTCCCGCGCCCCGAGCC	543	
Db	995	AAAAAASASASAVAV	VASSSSSSSSSSSSSSVSVSVSSSSCSVSVSVSSSS	1054	
QY	544	CCCGCGCCGCGGGGA	561		
Db	1055	VSVAVASASASVSSVA	1072		

RESULT 10
 CNS00720/c
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence T7 end of BAC #
 BACR14B09 of RPC1-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION
 VERSION
 AL066742
 KEYWORDS
 AL066742.1 GI:4945205
 SOURCE
 GSS.
 ORGANISM
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephyroidae; Drosophilidae; Drosophila.
 REFERENCE
 AUTHORS
 TITLE
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 JOURNAL
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 COMMENT
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutovo Osoeqawa and

BQ681076/c
 LOCUS BQ681076 1065 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT 8187867 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6259803
 5', mRNA sequence.
 ACCESSION BQ681076
 VERSION BQ681076.1 GI:21793755
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1065)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/BTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2417 row: 0 column: 04
 High quality sequence stop: 315.
 FEATURES
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 1..1065
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6259803"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 ORIGIN
 Query Match 13.2%; Score 74.4; DB 13; Length 1065;
 Best Local Similarity 45.4%; Pred. No. 0.0048;
 Matches 255; Conservative 0; Mismatches 305; Indels 2; Gaps 1;
 QY 2 GCGCGGAGCGCGCGGAGTGTGATCGTCTGCGCGCTCCACCTCCCGCAGGC 61
 Db 900 GGG 841
 QY 62 GCAGAGGCGGCCACGAGAGACCCCGAGTCCCGACGTTGCCACCGTCTGGGATCAGAGGC 121
 Db 840 GGG 781
 QY 122 AGGACACAGGAGCAGAGAACTGCGCGCGCCCGCCCTGCGCGCGAGGAGGAGCTC 181
 Db 780 GGG 721
 QY 182 CCTCACGAGGAGGAAGTTCCTCCACCGGCGCGAGCCCTGCGAGGGGGGGCGTGGGGTCA 241
 Db 720 GGGNGGGCGGGGGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGG 661
 QY 242 GACCGAAGCGAAGTGTGCGGGCGGGGTGGGCTTCGCGAGAGACAAAGCGCGGCGCTGCC 301
 Db 660 GGGGNGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 601
 QY 302 TCTCTCAGAGGGCCCCAGCGCTCCCAAGAGAGAGTCTCTCAGCGCCCGGCGAGAGGG 361
 Db 600 GCG--CCGGGGGGCGCGGGGCGGNGGGGGGGGGGGGGGGGGGGGGGG 543

QY 362 GGCACGCGCTTCCAGGGCCCGCGCGCGCGAGGAAAGTTGGCCAGGGCACGCGCGTGA 421
 Db 542 GGG 493
 QY 422 GCGAGCGCGGCGGCTTCTCAGAGCGCGGGCGGCGCGCTTGGAGGGCGAGGAC 481
 Db 482 CCGGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 423
 QY 482 CGGGTATAAGACCTCTGTCCTTCCCGGGCGAGCGCGAGGTTCCCGCGCGCGCGAG 541
 Db 422 GGG 363
 QY 542 CCGCGCGCGCGCGCGGGGAGG 563
 Db 362 GCGCGGG 341
 RESULT 13
 BQ6809572/c
 LOCUS BQ6809572 888 bp mRNA linear EST 22-MAY-2001
 DEFINITION mgct001xal4f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
 grisea cDNA clone mgct001xal4f 5', mRNA sequence.
 ACCESSION BQ6809572
 VERSION BQ6809572.1 GI:14180552
 KEYWORDS EST.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 888)
 Choi, W. and Dean, R.A.
 Construction and sequence analysis of an appressorium stage cDNA
 library in the rice blast fungus, Magnaporthe grisea
 Unpublished (2001)
 Contact: Ralph A. Dean
 Fungal Genomics Laboratory
 North Carolina State University
 Campus Box 7251, Raleigh, NC 27695, USA
 Tel: 919-513-0020
 Fax: 919-513-0024
 Email: ralph.dean@ncsu.edu
 Seq primer: T3 primer (AATTAACCTCTACTAAAGG).
 FEATURES
 source
 1..888
 Location/Qualifiers
 /organism="Magnaporthe grisea"
 /mol_type="mRNA"
 /strain="70-15"
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 /dev_stage="Germinated conidia on appressorium-inductive
 surface"
 /clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
 /note="Vector: pBlueScript SK(+) Vector; Site 1: EcoRI;
 Site 2: XhoI; The appressorium formation-specific cDNA
 library was constructed from conidia germinated for 5-8 hr
 on an inductive surface. The library contains over 55,000
 clones with average insert size of 1.5 kbp."
 ORIGIN
 Query Match 13.2%; Score 74.2; DB 12; Length 888;
 Best Local Similarity 49.5%; Pred. No. 0.005;
 Matches 213; Conservative 0; Mismatches 216; Indels 1; Gaps 1;
 QY 132 GAGCAGGAACTCGCGCGCGCGCGCGCGCTGCGCGGAGGAGCTCCCTCACCINCA 191
 Db 820 GCG 761
 QY 192 GGAAGCTCCCTCACCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 251
 Db 760 GGGCG 701
 QY 252 CGAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 311

source

1..949
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-021N08.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 13.1%; Score 73.6; DB 29; Length 949;
Best Local Similarity 44.9%; Fred. No. 0.0064;
Matches 225; Conservative 0; Mismatches 267; Indels 9; Gaps 2;
QY 57 CAGGCGCAGAGAGGCGCCACAGAGACCCAGTGCCTCCCGACGGTCTGGGATCA 116
Db 849 CGGGCGGCGCGCCGCCCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 790
QY 117 GAGGCGAGGACCGAGGAGCCAGGAACTGCGCGCGCCCGCGCGCGCGCGCGCG 176
Db 789 GGGCGGGGCG 730
QY 177 AGCTCCTCACGAGGAGAGCTCCCTCACCGCGCCCGCGCGCGCGCGCGCGCG 232
Db 729 GCG 670
QY 233 ---GTGGGGTCAAGCGCAAGAGTGCAGGCGCGGGCTCGCGGAGACAAAG 289
Db 669 GGGGGGGGCG 610
QY 290 GCGGGGCTGCTCTCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349
Db 609 GGNNGGCGGGGNGGNNNGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 550
QY 350 GCGAGGAGGGGCG 409
Db 549 GCGGNGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
QY 410 GCACGCGGTGAGCGGAGCGGGGCTTTCTCAGGAGCGCGGCGAGGCGCGCGCTGG 469
Db 491 GGGGGGCGGGGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432
QY 470 AGGGCGAGGACCGGGTATAGAGCCCTGCGGCGCTTCCCGGGGCGCGCGAGGTTCCCC 529
Db 431 CGCGCGGGGNGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372
QY 530 CG 550
Db 371 GGGGCGCGGGGCG 351

Search completed: June 6, 2004, 18:42:05
Job time : 2625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 15:41:42 ; Search time 406 Seconds
(without alignments)

5890.974 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence: 1 cggccggaggccgcccggg.....cccgccggccgcccggggagg 563

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001s:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298.4	53.0	1794	6	ABT06542 Human HIN
2	120	21.3	562	2	AAV54620 LU105 spe
3	117	20.8	190	2	AAV54616 LU105 spe
4	116	20.6	561	9	ADE39936 Human lun
5	92	16.3	543	3	AAZ29723 Human sig
6	92	16.3	543	3	AAZ298173 Human sig
7	78	13.9	519	2	AAV54621 LU105 pol
8	78	13.9	569	6	ABK40267 cDNA enco
9	78	13.9	570	3	AAZ65103 Membrane-
10	78	13.9	570	5	AAZ44249 Human PRO
11	78	13.9	570	7	ABX77974 Human PRO
12	78	13.9	570	7	ABX80386 Novel hum
13	78	13.9	570	7	ACA69292 Human cDN
14	78	13.9	570	7	ABX90363 Human sec
15	78	13.9	570	7	ABX64209 cDNA enco
16	78	13.9	570	7	ACA64431 Novel hum
17	78	13.9	570	7	ABX80890 Human sec
18	78	13.9	570	7	ACD44399 cDNA enco
19	78	13.9	570	7	ABX79570 Human sec
20	78	13.9	570	7	ACA93591 Novel hum
21	78	13.9	570	7	ABX81273 Novel hum
22	78	13.9	570	7	ACA93089 Novel hum
23	78	13.9	570	7	ABX17173 Human PRO

24	78	13.9	570	8	ACA68028	Novel hum
25	78	13.9	570	8	ACA88477	Human sec
26	78	13.9	570	8	ACD81984	CDNA enco
27	78	13.9	570	8	ADA37918	Human cDN
28	78	13.9	570	8	ADA21604	Human cDN
29	78	13.9	570	8	ADA10391	Human cDN
30	78	13.9	570	8	ADA17935	cDNA enco
31	78	13.9	570	8	ADA28043	Human cDN
32	78	13.9	570	8	ADA94623	Human cDN
33	78	13.9	570	8	ADA38848	Human cDN
34	78	13.9	570	8	ADA92969	Human cDN
35	78	13.9	570	8	ACH65545	Human cDN
36	78	13.9	570	8	ADA22530	Human cDN
37	78	13.9	570	8	ACD39535	Human cDN
38	78	13.9	570	8	ADA06696	Human sec
39	78	13.9	570	8	ADA39389	Human cDN
40	78	13.9	570	8	ADB96415	Human PRO
41	78	13.9	570	9	ADC57887	Human PRO
42	78	13.9	570	9	ADC55251	Human PRO
43	78	13.9	570	9	ADC12118	Human cDN
44	78	13.9	570	9	ADC56540	Human PRO
45	78	13.9	570	9	ADC07595	Human cDN

ALIGNMENTS

RESULT 1

ABT06542
ID ABT06542 standard; DNA; 1794 BP.

XX
AC ABT06542;

DT 07-NOV-2002 (first entry)

XX
Human HIN-1 coding sequence.

XX
Human; methylated gene; methylation; breast cancer; marker; WT-1;

KW cell proliferative disorder; TWIST; HOSAS; NES-1; PARbeta; cyclin D2;

KW retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;

KW 14.3.3 sigma; HIN-1; RASSF1A; tumour suppressor gene; hypermethylation;

KW gene; promoter; ds.

XX
Homo sapiens.

XX
WO200259347-A2.

XX
01-AUG-2002.

XX
28-JAN-2002; 2002WO-US002455.

XX
26-JAN-2001; 2001US-00771357.

XX
(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX
Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;

XX
WPI; 2002-599803/64.

XX
Diagnosing and/or determining a predisposition to a cellular

XX
proliferative disorder of breast tissue, in particular breast cancer, by

XX
determining the state of methylation of one or more nucleic acids

XX
isolated from the subject.

XX
Disclosure; Fig 9A; 115pp; English.

XX
The present invention relates to a method of diagnosing a cellular

XX
proliferative disorder of breast tissue, which involves determining the

XX
state of methylation of one or more nucleic acids isolated from the

XX
subject, where the state of methylation of the nucleic acids as compared

XX
with a state of methylation from a subject not having the cellular

XX
proliferative disorder of breast tissue is indicative of a cellular

XX
proliferative disorder of breast tissue in the subject. The nucleic acids

CC may be TWIST, HoxA5, NES-1, retinoic acid receptor beta (RARbeta),
 CC oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma,
 CC HTN-1 or RASSF1A. The method is useful for diagnosing and/or determining
 CC a predisposition to a cellular proliferative disorder, in particular
 CC breast cancer including ductal carcinoma in situ, lobular carcinoma,
 CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic
 CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and
 CC papillary carcinoma in situ. The present sequence is a gene fragment used
 CC in the exemplification of the invention
 XX
 XX Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 0 U; 68 Other;

Query Match 53.0%; Score 298.4; DB 6; Length 1794;
 Best Local Similarity 92.6%; Pred. No. 1.6e-48;
 Matches 302; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 226 GGGGCGGTGGGTTCAGACCGCAAGCAAGTCCGGGCGGGGTGGGCTTCGGGAGAC 285
 DB 846 GGGGCGGTGGGTTCAGACCGCAAGCAAGTCCGGGCGGGGTGGGCTTCGGGAGAC 905
 QY 286 AAAGCGCGGCTGCTCTCTCAGAGGGCCCCAGCGCTTCGCAAGAGGAAGTCTCTGAGG 345
 DB 906 AAAGCGCGGCTGCTCTCTCAGAGGGCCCCAGCGCTTCGCAAGAGGAAGTCTCTGAGG 965
 QY 346 CCGCGGCGAGGAAGGGCGACCGGCTTCCAGAGGCCCGCGCGCGAGCAAGTTGGC 405
 DB 966 CCGCGGCGAGGAAGGGCGACCGGCTTCCAGAGGCCCGCGCGCGAGCAAGTTGGC 1025
 QY 406 CAGGGACGCGCTGAGCGAGCGGGCAGGGCTTCTCAGAGCGGGCGAGGCGCGGCG 465
 DB 1026 CAGGGACGCGCTGAGCGAGCGGGCAGGGCTTCTCAGAGCGGGCGAGGCGCGGCG 1085
 QY 466 CTGAGGGCGGAGGACCGGGGTATAGAGGCTCTGTGGCTTGCCTGGCGGCGAGCGGTT 525
 DB 1086 CTGAGGGGNN 1145
 QY 526 CCG 551
 DB 1146 CCG 1171

RESULT 2
 AAV54620
 ID AAV54620 standard; cDNA; 562 BP.
 AC AAV54620;
 XX 25-MAR-2003 (revised)
 DT 30-OCT-1998 (first entry)
 XX LU105 specific consensus polynucleotide sequence.
 XX LU105; lung disease marker; immunoassay; lung disease; cancer; blood;
 KW plasma; serum; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 122..436
 FT /*tag=a
 FT /transl_except= (pos:176..178, aa:val)
 FT /product= "LU105 polypeptide"

PN WO9833926-A1.
 XX
 PD 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US001766.
 XX
 XX 31-JAN-1997; 97US-00791710.
 XX
 XX (ABBO) ABBOTT LAB.

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertstapp L;
 PI Russell JC, Stroupe SD;
 XX WPI; 1998-437479/37.
 DR P-PSDB; AAW75868.
 XX
 XX New nucleic acid for the lung disease marker LU105 - polypeptides,
 PT antibodies and genes, used for diagnosis, prevention, treatment of lung
 PT disease, specifically cancer.
 XX
 XX Claim 11; Fig 1; 123pp; English.

Sequences shown in AAV54616 to AAV54621 represent LU105 specific
 polynucleotide sequences. These are used in the method of the invention
 for detecting target LU105 nucleic acid. The method comprises treating a
 sample with at least one LU105 specific nucleic acid, or its complement
 which is at least 50 percent identical with the LU105 specific nucleic
 acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker.
 Cells transformed with a recombinant expression system that contains
 LU105 specific nucleic acid fragments, are used to express recombinant
 LU105 polypeptides which are used to raise antibodies. The antibodies are
 used to detect the LU105 antigen, and correspondingly this antigen is
 used to detect specific antibodies, in usual immunoassays. The LU105
 polypeptides and nucleic acid sequences are used for diagnosis, staging,
 monitoring, prognosis, prevention, treatment and determination of
 susceptibility to, lung disease, specifically cancer. The LU105
 polypeptides are also used to screen for specific binding agents, useful
 therapeutically, LU105 is a marker for lung disease (present at high
 concentration, in altered form or in an unusual body compartment). LU105
 can be detected in blood, plasma or serum in an inexpensive, non-invasive
 test. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 0 U; 2 Other;

Query Match 21.3%; Score 120; DB 2; Length 562;
 Best Local Similarity 99.2%; Pred. No. 2.8e-14;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 431 GCAGGGCTTCTCAGGAGCGCGGGCGAGGCGCGGCTGGAGGGCGAGGACCGGGTATAA 490
 DB 1 GCAGGGCTTCTCAGGAGCGCGGGCGAGGCGCGGCTGGAGGGCGAGGACCGGGTATAA 60
 QY 491 GAAGCTCTGTGGCTTCCCGGCGAGCCCGAGGTTCCCGCGCGCCCGAGCCCCCGCGC 550
 DB 61 GAAGCTCTGTGGCTTCCCGGCGAGCCCGAGGTTCCCGCGCGCCCGAGCCCCCGCGC 120
 QY 551 C 551
 DB 121 C 121

RESULT 3
 AAV54616
 ID AAV54616 standard; cDNA; 190 BP.
 AC AAV54616;
 XX 25-MAR-2003 (revised)
 DT 30-OCT-1998 (first entry)
 XX LU105 specific polynucleotide sequence from clone 3353867.
 XX LU105; lung disease marker; immunoassay; lung disease; cancer; blood;
 KW plasma; serum; ss.
 XX Homo sapiens.
 OS
 XX WO9833926-A1.
 XX
 XX 06-AUG-1998.
 XX
 XX 30-JAN-1998; 98WO-US001766.

XX 31-JAN-1997; 97US-00791710.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;
XX Russell JC, Stroupe SD;

XX WPI; 1998-437479/37.

XX New nucleic acid for the lung disease marker LUI05 - polypeptides,
XX antibodies and genes, used for diagnosis, prevention, treatment of lung
XX disease, specifically cancer.

XX Claim 11; Fig 1; 123pp; English.

XX Sequences shown in AAV54516 to AAV54621 represent LUI05 specific
XX polynucleotide sequences. These are used in the method of the invention
XX for detecting target LUI05 nucleic acid. The method comprises treating a
XX sample with at least one LUI05 specific nucleic acid, or its complement
XX which is at least 50 percent identical with the LUI05 specific nucleic
XX acid sequences (AAV54516 to AAV54621). LUI05 is a lung disease marker.
XX Cells transformed with a recombinant expression system that contains
XX LUI05 specific nucleic acid fragments, are used to express recombinant
XX LUI05 polypeptides which are used to raise antibodies. The antibodies are
XX used to detect the LUI05 antigen, and correspondingly this antigen is
XX used to detect specific antibodies, in usual immunoassays. The LUI05
XX polypeptides and nucleic acid sequences are used for diagnosis, staging,
XX monitoring, prognosis, prevention, treatment and determination of
XX susceptibility to, lung disease, specifically cancer. The LUI05
XX polypeptides are also used to screen for specific binding agents, useful
XX therapeutically. LUI05 is a marker for lung disease (present at high
XX concentration, in altered form or in an unusual body compartment). LUI05
XX can be detected in blood, plasma or serum in an inexpensive, non-invasive
XX test. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 0 U; 4 Other;

XX Query Match 20.8%; Score 117; DB 2; Length 190;

XX Best Local Similarity 96.7%; Pred. No. 1.1e-13;
XX Matches 117; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 431 GCAGGGCTTTCTCAGGAGCGCGGGCGAGCGCGCGTGGAGGGCGAGGACCGGGTATAA 49C
XX 1 GCAGGGCTTTCTCAGGAGCGCGGGCGAGCGCGCGTGGAGGGCGAGGACCGGGTATAA 60

XX 491 GAAGCCTCGTGGCCCTTGCCCGGCGAGCCGACGGTTCCTCCCGCGCCCGAGCCCGCGCG 550
XX 61 GAGGCTCGTGGCCCTTGCCCGGCGAGCCGACGGTTCCTCCCGCGCCCGAGCCCGCGCGC 120

XX 551 C 551

XX 121 C 121

XX RESULT 4
XX ADE39936
XX ID ADE39936 standard; cDNA; 561 BP.

XX ADE39936;

XX 29-JAN-2004 (first entry)

XX Human lung disorder-related cDNA - SEQ ID 6.

XX pepsin C; lung disorder; human; ss.

XX Homo sapiens.

XX US2003124580-A1.

XX 03-JUL-2003.

XX 06-SEP-2002; 2002US-00237435.

XX 07-SEP-2001; 2001US-0317822P.

XX (INCY-) INCYTE GENOMICS INC.

XX Walker MG, Spiro PA, Murry LE;

XX WPI; 2003-810982/76.

XX New cDNAs co-expressed with lung surfactant and surfactant synthesis
XX genes, useful as diagnostics in assessing the prognosis and treatment of
XX a lung disorder, or as potential targets for identifying therapeutics for
XX lung disorders.

XX Claim 2; SEQ ID NO 6; 29pp; English.

XX The invention relates to a novel isolated cDNA and a cDNA encoding pepsin
XX C. The polynucleotide of the invention may be useful as a probe or a
XX component within an expression vector, as a diagnostic in assessing the
XX prognosis and treatment of a lung disorder and as a potential therapeutic
XX or target for the identification of therapeutics for lung disorders.
XX Furthermore, the polynucleotide may be used to produce purified proteins
XX or peptides, which can subsequently be used to produce antibodies. The
XX current sequence is that of the human lung disorder-related cDNA (SEQ ID
XX 6) of the invention.

XX Sequence 561 BP; 86 A; 200 C; 189 G; 86 T; 0 U; 0 Other;

XX Query Match 20.6%; Score 116; DB 9; Length 561;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-13;

XX Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 436 GCTTCTCAGAGCGCGGCGAGCGCGCGTGGAGGGCGAGGACCGGGTATAAGAGC 495
XX 1 GCTTCTCAGAGCGCGGCGAGCGCGCGTGGAGGGCGAGGACCGGGTATAAGAGC 60

XX 496 CTCGTGGCCTTGGCCGCGAGCGCGAGTTCCTCCCGCGCCCGAGCCCGCGCGCC 551

XX 61 CTCGTGGCCTTGGCCGCGAGCGCGAGTTCCTCCCGCGCCCGAGCCCGCGCGCC 116

XX RESULT 5

XX AAZ29723

XX ID AAZ29723 standard; DNA; 543 BP.

XX AAZ29723;

XX 27-MAR-2000 (first entry)

XX Human lung specific gene Lng107.

XX Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;
XX lung cancer; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 93..407

XX /*tag= a

XX /product= "LSG Lng107 protein"

XX WO9960160-A1.

XX 25-NOV-1999.

XX 12-MAY-1999; 99WO-US010344.

XX 21-MAY-1998; 98US-0086212P.

XX (DIAD-) DIADEXUS LLC.

XX

```

PI Yang F, Macina RA, Sun Y;
XX
XX WPI: 2000-116320/10.
DR P-PSDB; AAY44458.
XX
PT A new method for diagnosing, monitoring and staging lung cancer.
PS
PS Claim 6; Page 36; 40pp; English.
XX
XX The present sequence is a lung specific gene (LSG) Lng107 from human
CC clone ID 586271. The LSG has high level of tissue specificity for lungs
CC and is overexpressed in cancerous tissues. The sequence serves as a
CC diagnostic marker for detecting, monitoring, staging and prognosticating
CC lung cancer. The diagnosis involves comparing levels of LSG in samples
CC obtained from patient and normal control
XX
SQ Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;
Query Match 16.3%; Score 92; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 6.7e-09;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 460 CCGCGCGCTGGAGGGCGGAGGACCGGGTATAGAGCCCTGCGTGGCTTGCCTCCGCGGCGAGCGG 519
Db 1 CCGGCGCTGGAGGGCGGAGGACCGGGTATAGAGCCCTGCGTGGCTTGCCTCCGCGGCGAGCGG 60
QY 520 CAGGTTCCCGCGCGCGCCCGAGCCCGCGCC 551
Db 61 CAGGTTCCCGCGCGCGCCCGAGCCCGCGCC 92
RESULT 6
RAZ98173
ID AAZ98173 standard; cDNA; 543 BP.
XX
AC AAZ98173;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-65 cDNA SEQ ID NO:199.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW anasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO20000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 98WO-US014484.
XX
PR 26-JUN-1998; 98US-0090762P.
PR 31-JUL-1998; 98US-0094983P.
PR 01-OCT-1998; 98US-0102686P.
PR 11-DEC-1998; 98US-0112129P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
DR P-PSDB; AAY87288.
XX

```

```

PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
XX disease.
XX Claim 9; Page 289; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
CC used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSP from natural
XX sources
XX
SQ Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;
Query Match 16.3%; Score 92; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 6.7e-09;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 460 CCGCGCGCTGGAGGGCGGAGGACCGGGTATAGAGCCCTGCGTGGCTTGCCTCCGCGGCGAGCGG 519
Db 1 CCGGCGCTGGAGGGCGGAGGACCGGGTATAGAGCCCTGCGTGGCTTGCCTCCGCGGCGAGCGG 60
QY 520 CAGGTTCCCGCGCGCGCCCGAGCCCGCGCC 551
Db 61 CAGGTTCCCGCGCGCGCCCGAGCCCGCGCC 92
RESULT 7
AAV54621
ID AAV54621 standard; cDNA; 519 BP.
XX
AC AAV54621;
XX
DT 25-MAR-2003 (revised)
DT 30-OCT-1998 (first entry)
XX
DE LUI05 polypeptide encoding cDNA clone 1327836IH.
XX
KW LUI05; lung disease marker; immunoassay; lung disease; cancer; blood;
KW plasma; serum; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
XX CDS 79..393
XX /*tag= a
XX /transl_except= (pos:136..138, aa:Val)
XX /product= "LUI05 polypeptide"
XX
XX WO9833926-A1.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US001766.
XX

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XX 31-JAN-1997; 97US-00791710.
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;
XX PI Russell JC, Stroupe SD;
XX
XX WPI; 1998-437479/37.
XX P-PSDB; AAW5868.
XX
XX New nucleic acid for the lung disease marker LU105 - polypeptides,
XX antibodies and genes, used for diagnosis, prevention, treatment of lung
XX disease, specifically cancer.
XX
XX Claim 11; Fig 1; 123pp; English.
XX
XX Sequences shown in AAV54616 to AAV54621 represent LU105 specific
XX polynucleotide sequences. These are used in the method of the invention
XX for detecting target LU105 nucleic acid. The method comprises treating a
XX sample with at least one LU105 specific nucleic acid, or its complement
XX which is at least 50 percent identical with the LU105 specific nucleic
XX acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker.
XX Cells transformed with a recombinant expression system that contains
XX LU105 specific nucleic acid fragments, are used to express recombinant
XX LU105 polypeptides which are used to raise antibodies. The antibodies are
XX used to detect the LU105 antigen, and correspondingly this antigen is
XX used to detect specific antibodies, in usual immunoassays. The LU105
XX polypeptides and nucleic acid sequences are used for diagnosis, staging,
XX monitoring, prognosis, prevention, treatment and determination of
XX susceptibility to, lung disease, specifically cancer. The LU105
XX polypeptides are also used to screen for specific binding agents, useful
XX therapeutically. LU105 is a marker for lung disease (present at high
XX concentration, in altered form or in an unusual body compartment). LU105
XX can be detected in blood, plasma or serum in an inexpensive, non-invasive
XX test. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
XX
XX Query Match 13.9%; Score 78; DB 2; Length 519;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-06;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 474 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGCAGCCGCGAGTTCCCGCGC 533
XX 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGCAGCCGCGAGTTCCCGCGC 60
XX
XX 534 GCCCGGAGCCCCCGCGCC 551
XX 61 GCCCGGAGCCCCCGCGCC 78
XX
XX RESULT 8
XX ID ABK40267
XX AC ABK40267;
XX
XX 15-JUL-2002 (first entry)
XX cDNA encoding human PRO1245 polypeptide.
XX
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
XX leukaemia; neuronal disorder; stromal disorder; blastocoelec disorder;
XX inflammatory disorder; immune disorder; angiogenic disorder;
XX gene therapy; cytostatic; neuroprotective; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200153486-A1.
XX 26-JUL-2001.
```

```
XX 11-FEB-2000; 2000WO-US003565.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 11-MAR-1999; 99US-0123972P.
XX 11-MAY-1999; 99US-0133459P.
XX 02-JUN-1999; 99WO-US012252.
XX 22-JUN-1999; 99US-0140650P.
XX 22-JUN-1999; 99US-0140653P.
XX 20-JUL-1999; 99US-0144758P.
XX 28-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 17-AUG-1999; 99US-0149395P.
XX 31-AUG-1999; 99US-0151689P.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 05-JAN-2000; 2000WO-US000219.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AU, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
XX Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
XX Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
XX P-PSDB; AAU86141.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
XX benign or malignant tumors, leukemias and lymphoid malignancies,
XX inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 50; Fig 27; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides and the polynucleotide sequences encoding them. The PRO
XX polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
XX treating benign or malignant tumors (e.g. renal, kidney, bladder,
XX breast, etc), leukaemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
XX stromal and blastocoelec disorders, inflammatory, immune and angiogenic
XX disorders. The polynucleotide sequences are also useful in gene therapy.
XX ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX
XX Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
XX
XX Query Match 13.9%; Score 78; DB 6; Length 569;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-06;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 474 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGCAGCCGCGAGTTCCCGCGC 533
XX 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGCAGCCGCGAGTTCCCGCGC 60
XX
XX 534 GCCCGGAGCCCCCGCGCC 551
XX 61 GCCCGGAGCCCCCGCGCC 78
XX
XX RESULT 9
XX ID AAZ65103
XX AC AAZ65103;
XX
XX 05-APR-2000 (first entry)
XX
XX Membrane-bound protein PRO1245 encoding cDNA.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.
```

XX OS	Homio sapiens.		
XX XX	WO9963088-A2.		
XX XX	09-DEC-1999.		
XX XX	02-JUN-1999;	99WO-US01252.	
PR PR	02-JUN-1998;	98US-0087607P.	98US-0090557P.
PR PR	02-JUN-1998;	98US-0087609P.	98US-0090676P.
PR PR	02-JUN-1998;	98US-0087759P.	98US-0090678P.
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PR PR	04-JUN-1998;	98US-0088021P.	98US-0090690P.
PR PR	04-JUN-1998;	98US-0088025P.	98US-0090691P.
PR PR	04-JUN-1998;	98US-0088028P.	98US-0090694P.
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PR PR	04-JUN-1998;	98US-0088033P.	98US-0090863P.
PR PR	04-JUN-1998;	98US-0088326P.	98US-0091358P.
PR PR	05-JUN-1998;	98US-0088167P.	98US-0091360P.
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PR PR	05-JUN-1998;	98US-0088212P.	98US-0091486P.
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PR PR	09-JUN-1998;	98US-0088655P.	98US-0091544P.
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PR PR	10-JUN-1998;	98US-0088825P.	98US-0095282P.
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PR PR	11-JUN-1998;	98US-0088858P.	98US-0095301P.
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PR PR	11-JUN-1998;	98US-0088876P.	98US-0095321P.
PR PR	12-JUN-1998;	98US-0089000P.	98US-0095325P.
PR PR	12-JUN-1998;	98US-0089105P.	98US-0096529P.
PR PR	16-JUN-1998;	98US-0089440P.	98US-0096757P.
PR PR	16-JUN-1998;	98US-0089512P.	98US-0096766P.
PR PR	16-JUN-1998;	98US-0089514P.	98US-0096768P.
PR PR	17-JUN-1998;	98US-0089532P.	98US-0096773P.
PR PR	17-JUN-1998;	98US-0089538P.	98US-0096791P.
PR PR	17-JUN-1998;	98US-0089598P.	98US-0096867P.
PR PR	17-JUN-1998;	98US-0089599P.	98US-0096891P.
PR PR	17-JUN-1998;	98US-0089600P.	98US-0096894P.
PR PR	18-JUN-1998;	98US-0089653P.	98US-0096895P.
PR PR	18-JUN-1998;	98US-0089801P.	98US-0096897P.
PR PR	18-JUN-1998;	98US-0089907P.	98US-0096949P.
PR PR	18-JUN-1998;	98US-0089908P.	98US-0096950P.
PR PR	19-JUN-1998;	98US-0089947P.	98US-0096959P.
PR PR	19-JUN-1998;	98US-0089948P.	98US-0096960P.
PR PR	22-JUN-1998;	98US-0090246P.	98US-0097022P.
PR PR	22-JUN-1998;	98US-0090252P.	98US-0097141P.
PR PR	22-JUN-1998;	98US-0090254P.	98US-0097218P.
PR PR	23-JUN-1998;	98US-0090349P.	98US-0097511P.
PR PR	23-JUN-1998;	98US-0090355P.	98US-009752P.
PR PR	24-JUN-1998;	98US-0090429P.	98US-0097954P.
PR PR	24-JUN-1998;	98US-0090431P.	98US-0097955P.
PR PR	24-JUN-1998;	98US-0090435P.	98US-0097971P.
PR PR	24-JUN-1998;	98US-0090444P.	98US-0097974P.
PR PR	24-JUN-1998;	98US-0090445P.	98US-0097978P.
PR PR	24-JUN-1998;	98US-0090461P.	98US-0097979P.
PR PR	24-JUN-1998;	98US-0090472P.	98US-0098014P.
PR PR	24-JUN-1998;	98US-0090535P.	98US-0098525P.
PR PR	24-JUN-1998;	98US-0090538P.	98US-0100634P.
PR PR	24-JUN-1998;	98US-0090540P.	99US-0115565P.
XX			XX

PA (GETH) GENENTECH INC.
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CX;
 PI Wood WI, Yuan J;
 XX
 DR WPI: 2000-072883/06.
 DR P-PSDB; AAY66757.
 XX
 XX Membrane-bound proteins and related nucleotide sequences.
 XX
 XX Claim 2; Fig 289; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques
 XX
 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
 Query Match 13.9%; Score 78; DB 3; Length 570;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 474 GCGAGGACCGGGTATAGAGCCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 533
 DB 1 GCGAGGACCGGGTATAGAGCCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 60
 QY 534 GCCCGGAGCCCCCGCGCC 551
 DB 61 GCCCGGAGCCCCCGCGCC 78
 XX
 RESULT 10
 AAF44249
 ID ID AAF44249 standard; cDNA; 570 BP.
 XX
 AC AAF44249;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1245 (UNQ629) nucleotide sequence SEQ ID NO:407.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
 KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US008439.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.

PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 02-MAR-2000; 2000WO-US005004.
 PR 15-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AU, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi CJ, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;
 XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 XX Zhang Z;
 XX WPI: 2001-032160/04.
 DR P-PSDB; AAB65280.
 XX
 XX PRO polynucleotides used to produce polypeptides used to target bioactive
 XX molecules such as toxins, radiolabels or antibodies, to specific cells,
 XX to cause targeted cell death.
 XX
 PS Claim 2; Fig 289; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
 Query Match 13.9%; Score 78; DB 5; Length 570;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 474 GCGAGGACCGGGTATAGAGCCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 533
 DB 1 GCGAGGACCGGGTATAGAGCCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 60
 QY 534 GCCCGGAGCCCCCGCGCC 551
 DB 61 GCCCGGAGCCCCCGCGCC 78
 XX
 RESULT 11
 ABX77974
 ID ABX77974 standard; cDNA; 570 BP.
 XX
 AC ABX77974;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human PRO polynucleotide #127.
 XX

KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027163-A1.

XX 06-FEB-2003.

XX 15-NOV-2001; 2001US-00397666.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

XX 28-APR-1998; 98US-0083322P.

XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087106P.

XX 02-JUN-1998; 98US-0087607P.

XX 02-JUN-1998; 98US-0087609P.

XX 03-JUN-1998; 98US-0087759P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

XX 04-JUN-1998; 98US-0088026P.

XX 04-JUN-1998; 98US-0088028P.

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98US-0096012P.

98US-0096143P.

24-JUN-1998;

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PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 17-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 12-MAR-1999; 98US-0123957P.
PR 02-JUN-1999; 98WO-US012252.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0143048P.
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PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 17-AUG-1999; 98US-0149396P.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98US-0158663P.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 16-DEC-1999; 98WO-US028634.
PR 01-DEC-1999; 98WO-US030095.
PR 16-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
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PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 13.9%; Score 78; DB 7; Length 570;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCCTCGTGGCTTGCCTGGCGGAGCGGAGGTTCCCGCGGC 533
Db 1 GCGAGGACCGGGTATAGAGCCTCGTGGCTTGCCTGGCGGAGCGGAGGTTCCCGCGGC 60

QY 534 GCCCGGACCGCGCGGC 551
Db 61 GCCCGGACCGCGCGGC 78

RESULT 12
ABX80386
ABX80386 standard; DNA; 570 BP.
XX ABX80386;
XX AC
XX XX
XX 28-APR-2003 (first entry)
XX Novel human secreted or transmembrane protein PRO1358 DNA.
XX DE
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX cardiac insufficiency disorder; cancer; tumor; immune response;
XX adrenal cortical capillary endothelial growth; c-Fos induction;
XX
```

```
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; genes; ds.
XX Homo sapiens.
OS US2002132252-A1.
PN 19-SEP-2002.
XX 14-NOV-2001; 2001US-00990442.
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088036P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 09-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088742P.
XX 10-JUN-1998; 98US-0088810P.
XX 10-JUN-1998; 98US-0088824P.
XX 10-JUN-1998; 98US-0088826P.
XX 11-JUN-1998; 98US-0088858P.
XX 11-JUN-1998; 98US-0088861P.
XX 11-JUN-1998; 98US-0088876P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089532P.
XX 17-JUN-1998; 98US-0089538P.
XX 17-JUN-1998; 98US-0089598P.
XX 17-JUN-1998; 98US-0089599P.
XX 17-JUN-1998; 98US-0089600P.
XX 17-JUN-1998; 98US-0089653P.
XX 18-JUN-1998; 98US-0089801P.
XX 18-JUN-1998; 98US-0089907P.
XX 18-JUN-1998; 98US-0089908P.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.
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PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P;
XX Grimaldi JC, Gurney AL, Kljavin IG, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
XX Zhang Z;

XX WPI; 2003-247083/24.
XX P-FSDB; AEU59174.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX are therapeutically useful for enhancing immune response and in cancer
XX treatments.

XX Claim 2; Fig 291; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be
XX beneficial, e.g. wound healing and antagonism of this polypeptide are
XX useful for treating cancerous tumours. PRO812 inhibits vascular
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
XX cells and is thus useful for inhibiting endothelial cell growth in
XX mammals which would be beneficial in inhibiting tumour growth. PRO26,
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
XX stimulated T-lymphocytes and are therapeutically useful for enhancing
XX immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of

CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD, PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide
XX

SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 13.9%; Score 78; DB 7; Length 570;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAAAGCTCTGTGGCTTGGCCGGCAGCGAGGTTCCCGCGC 533
|||
Db 1 GCGAGGACCGGGTATAGAAAGCTCTGTGGCTTGGCCGGCAGCGAGGTTCCCGCGC 60

QY 534 GCCCGAGCCCCCGGCC 551
|||
Db 61 GCCCGAGCCCCCGGCC 78

RESULT 13

ACA69292

ID ACA69292 standard; cDNA; 570 BP.

XX ACA69292;

XX 26-JUN-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1245.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;
XX cardiac insufficiency disorders; angiogenesis; wound healing;
XX cancerous tumour; immune response; retinal disorder; sight loss;
XX retinitis pigmentosum; age-related macular degeneration; AMD;
XX kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
XX Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX US2003032023-A1.

XX 13-FEB-2003.

XX 14-NOV-2001; 2001US-00990711.

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 03-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

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PR 24-AUG-1998; 98US-0097661P.
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PR 26-AUG-1998; 98US-0097986P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 12-MAR-1999; 98US-0123957P.
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PR 23-JUN-1999; 98US-0141037P.
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PR 20-JUL-1999; 98US-0144758P.
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PR 15-SEP-1999; 98WO-US021547.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 16-DEC-1999; 98WO-US028634.
PR 20-DEC-1999; 98WO-US030095.
PR 05-JAN-2000; 98WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.

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PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

    Query Match      13.9%; Score 78; DB 7; Length 570;
    Best Local Similarity 100.0%; Pred.No. 3.2e-06;
    Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGGACCGGGTATAGAGCCTTCGTCGCTTCGCGGCGAGCGCAGGTTCCCGCGC 533
Db 1 GCGAGGACCGGGTATAGAGCCTTCGTCGCTTCGCGGCGAGCGCAGGTTCCCGCGC 60

Qy 534 GCCCGGAGCCCCCGCGC 551
Db 61 GCCCGGAGCCCCCGCGC 78

RESULT 14
ABX90363 ID ABX90363 standard; cDNA; 570 BP.
AC ABX90363;
XX
XX DT DT (first entry)
XX 01-MAY-2003 (first entry)
XX Human secreted/transmembrane protein cDNA, #163.
XX
XX Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
XX pharmaceutical; diagnostic; therapeutic; gene therapy.
XX
XX Homo sapiens.
XX
XX US2002160384-A1.
XX
XX 31-OCT-2002.
XX
XX 14-NOV-2001; 2001US-00992598.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
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XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
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XX 04-JUN-1998; 98US-0088033P.
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XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.

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PR 10-JUN-1998; 98US-0088734P.
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PR 10-JUN-1998; 98US-0088824P.
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PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
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PR 12-JUN-1998; 98US-0089105P.
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PR 18-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
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PR 02-MAR-2000; 2000WO-US005004.
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PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
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PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
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PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

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(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Forg S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 Zhang Z;

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XX WPI; 2003-288106/28.
XX P-PSDB; ABU60604.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
XX PT polypeptides, useful in gene therapy, in chromosome identification, as
XX PT chromosome markers, or in generating probes.
XX
XX Claim 2; Fig 289; 650pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX CC comprising a sequence without signal peptide and the nucleic acid
XX CC encoding them. The polypeptides can be used to raise antibodies that
XX CC specifically bind to the PRO polypeptide, for linking a bioactive
XX CC molecule to a cell expressing a PRO protein and for modulating at least
XX CC one biological activity of a cell. The PRO polypeptides or
XX CC polynucleotides are also useful in gene therapy, in chromosome
XX CC identification, as chromosome markers, or in generating probes. The PRO
XX CC polypeptides are useful as molecular markers for protein electrophoresis,
XX CC and the isolated nucleic acids may be used for recombinantly expressing
XX CC those markers. The PRO polypeptides and nucleic acids may also be used in
XX CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
XX CC PRO, and in affinity purification of PRO from recombinant cell culture or
XX CC natural sources. The sequences presented in ABX90083-ABX90468 are the
XX CC genes encoding, the primers amplifying and the probes detecting the PRO
XX CC polynucleotides of the invention. Note: The sequence data for this patent
XX CC is also available in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
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XX Query Match 13.9%; Score 78; DB 7; Length 570;
XX Best Local Similarity 100.0%; Pred.No. 3.2e-06;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCGAGGACCGGTATAGACGCTTGCGCGGCGAGCGCGAGGTTCGCCGCGC 60
Qy 534 GCCCGAGCCCCCGGCC 551
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XX AC ABX64209;
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XX DT 26-FEB-2003 (first entry)
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XX
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;
XX KW genetic disorder; antibacterial; immunosuppressive; transgenic;
XX KW gene therapy; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2002103125-A1.
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XX PD 01-AUG-2002.
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XX PF 20-NOV-2001; 2001US-00989731.
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XX 16-JUN-1997; 97US-0049787P.
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XX 17-OCT-1997; 97US-0062250P.
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XX 05-NOV-1997; 97WO-US020069.
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XX 12-NOV-1997; 97US-0065186P.
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XX 13-NOV-1997; 97US-0065311P.
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XX 24-NOV-1997; 97US-0066770P.
XX
XX 25-FEB-1998; 98US-0075945P.
102-MAR-1998; 98US-0078910P.
28-APR-1998; 98US-0083322P.
07-MAY-1998; 98US-0084600P.
28-MAY-1998; 98US-0087106P.
02-JUN-1998; 98US-0087607P.
02-JUN-1998; 98US-0087609P.
02-JUN-1998; 98US-0087759P.
03-JUN-1998; 98US-0087827P.
04-JUN-1998; 98US-0088021P.
04-JUN-1998; 98US-0088025P.
04-JUN-1998; 98US-0088026P.
04-JUN-1998; 98US-0088028P.
04-JUN-1998; 98US-0088029P.
04-JUN-1998; 98US-0088030P.
04-JUN-1998; 98US-0088033P.
04-JUN-1998; 98US-0088326P.
05-JUN-1998; 98US-0088167P.
05-JUN-1998; 98US-0088202P.
05-JUN-1998; 98US-0088212P.
05-JUN-1998; 98US-0088217P.
09-JUN-1998; 98US-0088655P.
10-JUN-1998; 98US-0088734P.
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12-JUN-1998; 98US-0089440P.
16-JUN-1998; 98US-0089512P.
16-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089532P.
17-JUN-1998; 98US-0089538P.
17-JUN-1998; 98US-0089598P.
17-JUN-1998; 98US-0089599P.
17-JUN-1998; 98US-0089600P.
17-JUN-1998; 98US-0089653P.
18-JUN-1998; 98US-0089801P.
18-JUN-1998; 98US-0089907P.
18-JUN-1998; 98US-0089908P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
06-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
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PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH) GENENTECH LTD.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski Pu;
PI Grimaldi JC, Gurney AL, Klijavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-102117/09.
DR P-PSDB; ABU13986.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
FT antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 2; Fig 289; 649pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 13.9%; Score 78; DB 7; Length 570;
Best Local Similarity 100.0%; Pred.No. 3.2e-06;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGACCTCGTCCCTTCCCGCGAGCGGAGGTTCCCGCGC 533
Db 1 GCGAGGACCGGGTATAGACCTCGTCCCTTCCCGCGAGCGGAGGTTCCCGCGC 60

QY 534 GCCCGAGCGCCCGCGCC 551
Db 61 GCCCGAGCGCCCGCGCC 78

Search completed: June 6, 2004, 16:54:37
Job time : 406 secs

GenCore version 5.1.6
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DM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 15:43:12 ; Search time 3796 Seconds
(without alignments)
6428.379 Million cell updates/sec

Title: SEQ19PLUS12
Perfect score: 563
Sequence: 1 cggccggggagcggccggg.....cccgccggccggggagg 563

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 13: gb_un.*
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- 15: em_ba.*
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- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
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- 24: em_ph.*
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- 27: em_sts.*
- 28: em_un.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rnd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	488.6	86.8	127488	2	AC022095	AC022095 Homo sapi
C 2	486	86.3	168347	2	AC025336	AC025336 Homo sapi
C 3	486	86.3	190024	9	AC122714	AC122714 Homo sapi
C 4	478.8	85.0	130129	2	AC108083	AC108083 Homo sapi
5	475	84.4	166777	2	AC106813	AC106813 Homo sapi
6	120	21.3	562	6	BD082141	BD082141 Reagents
7	117	20.8	190	6	BD082137	BD082137 Reagents
8	92	16.3	543	6	BD222719	BD222719 Human sig
9	92	16.3	543	6	BD226775	BD226775 A novel m
10	78	13.9	519	6	BD082142	BD082142 Reagents
11	78	13.9	569	6	AX201348	AX201348 Sequence
12	78	13.9	570	6	AR252648	AR252648 Sequence
13	78	13.9	570	6	AX403520	AX403520 Sequence
14	78	13.9	570	9	AY359064	AY359064 Homo sapi
15	77	13.7	244	6	BD082138	BD082138 Reagents
C 16	74.4	13.2	172650	2	AF005772	AF005772 Oryza sat
C 17	74	13.1	125020	9	AF429315	AF429315 Homo sapi
C 18	70	12.4	1279	11	PM2H12G	AL684840 Penicilli
19	69	12.3	138709	2	BX649540	BX649540 Danio rer
20	68	12.1	167624	2	AC143286	AC143286 Macaca mu
C 21	68	12.1	219952	2	AC084804	AC084804 Mus muscu
22	67.4	12.0	63082	2	AC022663	AC022663 Homo sapi
23	67.2	11.9	183305	2	BX640474	BX640474 Danio rer
24	67	11.9	991	11	PM12H12B	AL684455 Penicilli
C 25	64.8	11.5	63082	2	AC022663	AC022663 Homo sapi
C 26	64.6	11.5	1094	11	PM7G11B	AL685196 Penicilli
C 27	64.2	11.4	240957	9	AC011407	AC011407 Homo sapi
28	63.8	11.3	1052	11	PM2H12B	AL684839 Penicilli
29	63.6	11.3	101509	2	AC027353	AC027353 Homo sapi
C 30	63.2	11.2	1007	11	PM3H11G	AL685749 Penicilli
C 31	63	11.2	65351	2	AC139773	AC139773 Homo sapi
32	62.8	11.2	956	11	PM2D12B	AL684743 Penicilli
33	62.4	11.1	125020	9	AF429315	AF429315 Homo sapi
C 34	62.2	11.0	129506	2	AC136100	AC136100 Rattus no
35	62.2	11.0	181850	2	BX276102	BX276102 Danio rer
C 36	62.2	11.0	224777	2	AC138109	AC138109 Mus muscu
37	62	11.0	154890	2	BX548249	BX548249 Danio rer
C 38	61.8	11.0	976	11	PM12D6G	AL684370 Penicilli
C 39	61.8	11.0	72645	2	AC112672	AC112672 Mus muscu
C 40	61.8	11.0	187413	2	AC141871	AC141871 Mus muscu
41	61.6	10.9	1965	10	AF411253	AF411253 Mus muscu
C 42	61.6	10.9	167077	2	AC091093	AC091093 Papio anu
C 43	61.4	10.9	239130	2	AC079420	AC079420 Mus muscu
C 44	60.8	10.8	885	11	PM7F8G	AL685189 Penicilli
45	60.6	10.8	1065	11	PM2B12B	AL684695 Penicilli

ALIGNMENTS

RESULT 1
AC022095/c
LOCUS AC022095 127488 bp DNA linear HTG 20-APR-2001
DEFINITION Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,
13 unordered pieces.
ACCESSION AC022095
VERSION AC022095.5 GI:13699618
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5


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81129 GGGGACGGGCTTCCCGAGGGCCCGCGCCGACGAGGAAAGTTGGCCAGGACACGGCCGT 81070
420 CAGCGGAGCGGCGAGGCTTTCTCAGGAGCGCGCGGCGGCGGCTGGAGGCGGCGAGG 479
81069 GAGCGGAGCGGCGAGGCTTTCTCAGGAGCGCGCGGCGGCGGCTGGAGGCGGCGAGG 81010
480 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGGCAGCGCAGGTTCCCGCGGCGCCCG 539
81009 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGGCAGCGCAGGTTCCCGCGGCGCCCG 80950
540 AGCCCCCGGCC 551
80949 AGCCCCCGGCC 80938

RESULT 4
AC108083/3
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
ACCESSION AC108083
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Unpublished
2 (bases 1 to 130129)
DOE Joint Genome Institute.
Direct Submission
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

-----
Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 12922 bp in length
* 23712 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
Location/Qualifiers
1..130129
/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN

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Query Match 85.0%; Score 478.8; DB 2; Length 130129;
Best Local Similarity 95.3%; Pred. No. 1.3e-70;
Matches 522; Conservative 0; Mismatches 7; Indels 19; Gaps 2;

QY 1 CGCGCGGGAGGCGCGGAGTGAAGCTTATCGTCTCGCTGGCGCCTCCACCTCCCGAGG 60
Db CGCGCGGGAGGCGCGGAGTGAAGCTTATCGTCTCGCTGGCGCCTCCACCTCCCGAGG 24510
QY 61 CGCAGAAAGGCGCCACGAGGACCCCGAGTGCCTCCGACGCTTGCACGGTCTGGATCAGAGG 120
Db CGCAGAAAGGCGCCACGAGGACCCCGAGTGCCTCCGACGCTTGCACGGTCTGGATCAGAGG 24450
QY 121 CAGGACACGAGGACCGAGGAACCTGCGCGCGCCCGCCCTGCTCCCTGGCGGAGGAAGCT 180
Db CAGGACACGAGGACCGAGGAACCTGCGCGCGCCCGCCCTGCTCCCTGGCGGAGGAAGCT 24390
QY 181 CCCTCACGNGAGGGAAGCTCCCTCACCAGCGCCCGAGCCCTGCGAGGGGGGCGCTGGGGTC 240
Db 24389 C-----CCCTCACCGCGCGCCAGCCCTGCGAGGGGGGCGCGTGGGGTC 24348
QY 241 AGACCGCAAGCGAAGGTGCGGGCGGGGTGGGCTCGCGGAGACAAAGCCGGGCGCTGC 300
Db 24347 AGACCGCAAGCGAAGGTGCGGGCGGGGTGGGCTCGCGGAGACAAAGCCGGGCGCTGC 24288
QY 301 CT-CTCTCAGAGGCGCCCGAGCGCTGCCAAGAGGAAGTCTCTCGAGGCCCGGGCAGGGAAG 359
Db 24287 CTGCTCTCAGAGGCGCCCGAGCGCTGCCAAGAGGAAGTCTCTCGAGGCCCGGGCAGGGAAG 24228
QY 360 GGGGACAGGGCTTCCAGAGGCCCGCGCGCGAGGAAAGTTGGCCAGGCGACGGCCGT 419
Db 24227 GGGGACAGGGCTTCCAGAGGCCCGCGCGCGAGGAAAGTTGGCCAGGCGACGGCCGT 24168
QY 420 GAGCGGAGCGGGCAGGCGCTTCTCAGAGGCGCGGGCGAGCGCGCTGAGGGGGCGAGG 479
Db 24167 GAGCGGAGCGGGCAGGCGCTTCTCAGAGGCGCGGGCGAGCGCGCTGAGGGGGCGAGG 24108
QY 480 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGGCAGCGCAGGTTCCCGCGCGCCCG 539
Db 24107 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGGCAGCGCAGGTTCCCGCGCGCCCG 24048
QY 540 AGCCCCCG 547
Db 24047 AGCCCCCG 24040

RESULT 5
AC106813
LOCUS
DEFINITION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
3 ordered pieces.
ACCESSION AC106813
VERSION AC106813.3 GI:19224876
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166777)
DOE Joint Genome Institute.
Unpublished
2 (bases 1 to 166777)
DOE Joint Genome Institute.
Direct Submission
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE
3 (bases 1 to 166777)
DOE Joint Genome Institute.
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TITLE JOURNAL COMMENT

Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 7, 2002 this sequence version replaced gi:18369924.

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1519801
Center clone name: RPCI-11_586L9

Summary Statistics
Consensus quality: 163497 bases at least Q40
Consensus quality: 166071 bases at least Q30
Consensus quality: 166432 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 166577; sum-of-ctnigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 10.51 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 62237: contig of 62237 bp in length
* 62238 62337: gap of unknown length
* 62338 75837: contig of 13500 bp in length
* 75838 75937: gap of unknown length
* 75938 166777: contig of 90840 bp in length.
* Location/Qualifiers

FEATURES source

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/mol_type="genomic DNA"
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ORIGIN

Query Match 84.4%; Score 475; DB 2; Length 166777;
Best Local Similarity 95.5%; Pred. No. 5.2e-70;
Matches 528; Conservative 0; Mismatches 5; Indels 20; Gaps 3;
QY 1 CGGCCGGGAGGCGCGGAGTGTAGGCTGTATGCTCTGCGGCTCCACTCCCGAGG 60
DB 119104 CGGCCGGGAGGCGCGGAGTGTAGGCTGTATGCTCTGCGGCTCCACTCCCGAGG 119163
QY 61 CGCAGAAGCGCCACGAGGACCCCGAGTCCCGGACGTTGCCACGCTCTGGATCAGAGG 120
DB 119164 CGCAGAAGCGCCACGAGGACCCCGAGTCCCGGACGTTGCCACGCTCTGGATCAGAGG 119223
QY 121 CAGGGACAGGAGGAGGAGTGGCGCCCGCCCGCCCTGCGGCGGAGGGAAGCT 180
DB 119224 CAGGGACAGGAGGAGGAGTGGCGCCCGCCCGCCCTGCGGCGGAGGGAAGCT 119283
QY 181 CCCTCACCNGAGGAGTCCCTCTACCCGCGCCGACGCTCTGAGGGGGCGGCTGGGTC 240
DB 119284 C-----CCCTCACCNGAGGAGTCCCTCTACCCGCGCCGACGCTCTGAGGGGGCGGCTGGGTC 119325
QY 241 AGACCGCAAGCGAAGGTTCGGGCGCGGGTGGGCTTCGGGAGACAAAGGCCGCGCTCC 300
DB 119326 AGACCGCAAGCGAAGGTTCGGGCGCGGGTGGGCTTCGGGAGACAAAGGCCGCGCTTC 119385
QY 301 CT-CTCTCAGAGGGGCCCGCCAGCGCTTCGCCAAGAGGAAGTCTTCAGGCGCCGGGACGGAAG 359
DB 119386 CTGCTCTCAGAGGGGCCCGCCAGCGCTTCGCCAAGAGGAAGTCTTCAGGCGCCGGGACGGAAG 119445

QY 360 GGGGCACGGGCTTCCAGGGCCCGCCGCGCAGCAGGAAGTTGGCCAGGCGCAGGCGGT 419
DB 119446 GGGGCACGGGCTTCCAGGGCCCGCCGCGCAGCAGGAAGTTGGCCAGGCGCAGGCGGT 119505
QY 420 GAGCGGAGCGGCGAGGCTTTCTCAGGAGCGCGGGCGGCGGCGCTGTGAGGGG-CGAG 478
DB 119506 GAGCGGAGCGGCGAGGCTTTCTCAGGAGCGCGGGCGGCGGCGCTGTGAGGGGCGAG 119565
QY 479 GACCGGTATAGAGGCTCTGCGGCTTCCCGGGCAGCGCAGGTTCCCGCGCGGCCCC 538
DB 119566 GACCGGTATAGAGGCTCTGCGGCTTCCCGGGCAGCGCAGGTTCCCGCGCGGCCCC 119625
QY 539 GAGCGCGCGCGCC 551
DB 119626 GAGCGCGCGCGCC 119638

RESULT 6

BD082141
LOCUS
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION BD082141
VERSION BD082141.1 GI:22627751
KEYWORDS JP 2001522225-A/5.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 562)
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
Russell,J.C. and Stroupe,S.D.
TITLE Reagents and methods useful for detecting diseases of the lung
JOURNAL Patent: JP 2001522225-A 5 13-NOV-2001;
ABBOTT LABORATORIES
COMMENT FN JP 2001522225-A/5
PD 13-NOV-2001
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA

PI N FRIEDMAN,
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
KLASS,
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
PI STROUPE
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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1..562
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/mol_type="genomic DNA"
/db_xref="taxon:4577"

ORIGIN

Query Match 21.3%; Score 120; DB 6; Length 562;
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Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 GCAGGGCTTTCTCAGGNGCGCGGCGGCGGCGCTGAGGGGCGGAGCCGGGTATAA 60
QY 491 GAAGCTTGTGGCTTGCCTGGGCGAGCGCGAGGTTCCCGGCGCCCGAGCCCGCGC 550
DB 61 GAAGCTTGTGGCTTGCCTGGGCGAGCGCGAGGTTCCCGGCGCCCGAGCCCGCGC 120
QY 551 C 551
DB 121 C 121

RESULT 7
 BD082137
 LOCUS
 DEFINITION
 HUMAN signal peptide-containing protein.
 ACCESSION
 BD082137
 VERSION
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 KEYWORDS
 JP 2001522225-A/1.
 SOURCE
 Zea mays
 ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 190)
 Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
 Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,
 Russell, J.C. and Stroupe, S.D.
 Reagents and methods useful for detecting diseases of the lung
 Patent: JP 2001522225-A 1 13-NOV-2001;
 ABBOTT LABORATORIES
 PN JP 2001522225-A/1
 PD 13-NOV-2001
 PF 30-JAN-1998 JP 1998533078
 PR 31-JAN-1997 US 08/791710
 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
 N FRIEDMAN,
 JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
 KLASS,
 JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
 STROUPE
 PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
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 CC Topology: Linear;
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 Ddb 121 C 121
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 LOCUS
 DEFINITION
 Human signal peptide-containing protein.
 ACCESSION
 BD222719
 VERSION
 1
 KEYWORDS
 JP 2002519030-A/65.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 543)
 Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J.,
 Y. E., Young, J.A., Yue, H., Patterson, C.,
 Hillman, J.L. and Bandman, O.
 Human signal peptide-containing protein
 Patent: JP 2002519030-A 65 02-JUL-2002;
 INCYTE PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002519030-A/65
 PD 02-JUL-2002
 PF 25-JUN-1999 JP 2000557363
 PR 26-JUN-1998 US 60/090762 31-JUL-1998 US 60/094983 PR
 01-OCT-1998 US 60/102686 11-DEC-1998 US 60/112129 PI PREETI
 LAL, Y. TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,
 MARIAM R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,
 CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN
 PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61P9/00, A61P15/00,
 A61P25/00,
 PC A61P29/00, A61P35/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, PC
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 PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//C12P21/08, PC
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 Ddb 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCC 92
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 LOCUS
 DEFINITION
 A novel method of diagnosing, monitoring and staging lung cancer.
 ACCESSION
 BD226775
 VERSION
 1
 KEYWORDS
 JP 2002515262-A/6.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 543)
 Yang, F., Macina, R.A. and Sun, Y.
 A novel method of diagnosing, monitoring and staging lung cancer
 Patent: JP 2002515262-A 6 28-MAY-2002;
 DIADEXUS INC
 OS Homo sapiens (human)
 PN JP 2002515262-A/6
 PD 28-MAY-2002
 PF 12-MAY-1999 JP 2000549766
 PR 21-MAY-1998 US 60/086212
 PI FEI YANG, ROBERTO A MACINA, YONGMING SUN
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Baughn, M.R., Akerblom, I.E., Young, J.A., Yue, H., Patterson, C.,
 Reddy, R., Hillman, J.L. and Bandman, O.
 Human signal peptide-containing protein
 Patent: JP 2002519030-A 65 02-JUL-2002;
 INCYTE PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002519030-A/65
 PD 02-JUL-2002
 PF 25-JUN-1999 JP 2000557363
 PR 26-JUN-1998 US 60/090762 31-JUL-1998 US 60/094983 PR
 01-OCT-1998 US 60/102686 11-DEC-1998 US 60/112129 PI PREETI
 LAL, Y. TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,
 MARIAM R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,
 CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN
 PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61P9/00, A61P15/00,
 A61P25/00,
 PC A61P29/00, A61P35/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, PC
 C12N1/19,
 PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//C12P21/08, PC
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 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 460 CCGCGCTGGAGGGCGAGGACCGGGTATAGAGCCTCGTGGCTTCCCGGCGAGCGG 519
 Ddb 1 CCGCGCTGGAGGGCGAGGACCGGGTATAGAGCCTCGTGGCTTCCCGGCGAGCGG 60
 QY 520 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCC 551
 Ddb 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCC 92
 RESULT 9
 BD226775
 LOCUS
 DEFINITION
 A novel method of diagnosing, monitoring and staging lung cancer.
 ACCESSION
 BD226775
 VERSION
 1
 KEYWORDS
 JP 2002515262-A/6.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 543)
 Yang, F., Macina, R.A. and Sun, Y.
 A novel method of diagnosing, monitoring and staging lung cancer
 Patent: JP 2002515262-A 6 28-MAY-2002;
 DIADEXUS INC
 OS Homo sapiens (human)
 PN JP 2002515262-A/6
 PD 28-MAY-2002
 PF 12-MAY-1999 JP 2000549766
 PR 21-MAY-1998 US 60/086212
 PI FEI YANG, ROBERTO A MACINA, YONGMING SUN
 PC C12N15/09, C12Q1/68, G01N33/50, C12N15/00
 CC A novel method of diagnosing, monitoring and staging lung CC
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 FH Key Location/Qualifiers
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QY	520	CAGGTTCCCGCGCGCCCGAGCCCCCGGCC	551				
Db	61	CAGGTTCCCGCGCGCCCGAGCCCCCGGCC	92				
RESULT 10							
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LOCUS							
DEFINITION							Reagents and methods useful for detecting diseases of the lung.
ACCESSION							BD082142
VERSION							BD082142.1
KEYWORDS							GI:22627752
SOURCE							JP 2001522225-A/6.
ORGANISM							Zea mays
REFERENCE							1 (bases 1 to 519)
AUTHORS							Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
TITLE							Medel,P.A.B., Cohen,X., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
JOURNAL							Reagents and methods useful for detecting diseases of the lung
COMMENT							Patent: JP 2001522225-A 6 13-NOV-2001; ABBOTT LABORATORIES
FN							JP 2001522225-A/6
PD							13-NOV-2001
PF							30-JAN-1998 JP 1998533078
PR							31-JAN-1997 US 08/791710
PI							PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA N FRIEDMAN, JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI KLASS,
PI							JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D STROUBE
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Db	61	GCCCCGAGCCCCCGGCC	78				
RESULT 11							
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LOCUS							
DEFINITION							Sequence 27 from Patent WO0153486.
ACCESSION							AX201348
VERSION							AX201348.1
KEYWORDS							GI:15391167
SOURCE							Homo sapiens (human)
ORGANISM							Homo sapiens
REFERENCE							1
AUTHORS							Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE							Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V., Stone,D.M., Watanabe,C.K. and Wood,W.I.
JOURNAL							Compositions and methods for the treatment of tumour
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QY	534	GCCCCGAGCCCCCGGCC	551				
Db	61	GCCCCGAGCCCCCGGCC	78				
RESULT 12							
AR252648			570 bp	DNA	linear		PAT 20-DEC-2002

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RESULT 13
LOCUS AX403520
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION AX403520
VERSION AX403520.1 GI:21437002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ferrata,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J., Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0073454-A 407 07-DEC-2000;
Genentech Inc. (US)
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Db 61 GCGGCGAGCGGCGGCGC 78
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LOCUS AY359064
DEFINITION Homo sapiens clone DNA64884 SCGB3A1 (UNQ629) mRNA, complete cds.
ACCESSION AY359064
VERSION AY359064.1 GI:37183245
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a large-scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 570)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Db 61 GCGGCGAGCGGCGGCGC 78
RESULT 15
LOCUS BD082138
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION BD082138
VERSION BD082138.1 GI:22627748
KEYWORDS JP 2001522225-A/2.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE Reagents and methods useful for detecting diseases of the lung
JOURNAL Patent: JP 2001522225-A 2 13-NOV-2001;
COMMENT ABBOTT LABORATORIES
PN JP 2001522225-A/2
PD 13-NOV-2001
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA N FRIEDMAN,
PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI
KLAAS,
PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
STROUPE
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